

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:17:47 ; Search time 53.3338 Seconds
(without alignments)
1348.171 Million cell updates/sec

Title: US-09-802-077-8

Perfect score: 2432

Sequence: 1 EVOLVESGGGLVPGGSLRL.....MHEALHHYTKRSLSPGK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 2432 | 100.0 | 453 | 14 AAR33311 | Humanised MaE11 Ve |
| 2 | 2432 | 100.0 | 453 | 21 AAR85199 | Heavy chain amino |
| 3 | 2391 | 98.3 | 451 | 20 AAW95659 | Mus musculus anti- |
| 4 | 2391 | 98.3 | 451 | 20 AAW95661 | Mus musculus anti- |
| 5 | 2391 | 98.3 | 451 | 21 AAY85201 | Light chain amino |
| 6 | 2391 | 98.3 | 451 | 22 AAB47088 | Anti-IgE antibody, |
| 7 | 2391 | 98.3 | 451 | 22 AAB76948 | Full length heavy |
| 8 | 2391 | 98.3 | 451 | 22 AAB76950 | Full length heavy |
| 9 | 2369 | 97.4 | 451 | 20 AAY50031 | Human E27 anti-IgE |

| | | | | | |
|----|--------|------|-----|-------------|--------------------|
| 10 | 2369 | 97.4 | 451 | 20 AAW95663 | Mus musculus anti- |
| 11 | 2369 | 97.4 | 451 | 21 AAB07473 | Amino acid sequenc |
| 12 | 2369 | 97.4 | 451 | 22 AAB74212 | E27 anti-IgE antib |
| 13 | 2369 | 97.4 | 451 | 22 AAB76952 | Full length heavy |
| 14 | 2214.5 | 91.1 | 452 | 20 AAY29458 | Recombinant immuno |
| 15 | 2214.5 | 91.1 | 452 | 21 AAB30322 | Humanised anti-IL- |
| 16 | 2214.5 | 91.1 | 452 | 21 AAY77766 | Humanised anti-IL- |
| 17 | 2214.5 | 91.1 | 452 | 24 ABU59512 | Humanised Mouse an |
| 18 | 2214.5 | 91.1 | 452 | 24 ABU13799 | Humanised mouse an |
| 19 | 2210 | 90.9 | 476 | 23 ABB81110 | Anti-VEGF heavy ch |
| 20 | 2207.5 | 90.8 | 447 | 24 AAE33522 | Human AOC2 heavy c |
| 21 | 2205.5 | 90.7 | 452 | 19 AAW69316 | Anti-IL-8 humanise |
| 22 | 2204.5 | 90.6 | 477 | 22 AAU14288 | Human novel protei |
| 23 | 2201.5 | 90.5 | 447 | 24 AAE33523 | Human AOC2 heavy c |
| 24 | 2197.5 | 90.4 | 447 | 24 AAE33524 | Human AOC2 heavy c |
| 25 | 2191 | 90.1 | 449 | 24 ABP58273 | Humanised 3D6 anti |
| 26 | 2191 | 90.1 | 468 | 24 ABP58275 | Humanised 3D6 anti |
| 27 | 2183.5 | 89.8 | 475 | 13 AAR20057 | Heavy chain of 3D6 |
| 28 | 2182 | 89.7 | 449 | 21 AAY68810 | A rat heavy chain |
| 29 | 2178 | 89.6 | 474 | 23 AAO14065 | Heavy chain protei |
| 30 | 2178 | 89.6 | 474 | 24 ABU08017 | Human monoclonal r |
| 31 | 2177.5 | 89.5 | 444 | 24 AAE34876 | BIWA4/8 antibody h |
| 32 | 2177 | 89.5 | 451 | 22 AAE12715 | Human recombinant |
| 33 | 2177 | 89.5 | 451 | 24 ABU58807 | Mucin 1 (MUC-1) bi |
| 34 | 2176.5 | 89.5 | 442 | 24 ABB80109 | Heavy chain. Homo |
| 35 | 2176.5 | 89.5 | 442 | 24 ABR39465 | Humanised anti-Abe |
| 36 | 2176.5 | 89.5 | 442 | 24 ABU08311 | Humanised 266 anti |
| 37 | 2176.5 | 89.5 | 461 | 22 AAU07745 | Humanised monoclon |
| 38 | 2170.5 | 89.2 | 449 | 23 AAO18400 | Mature humanised m |
| 39 | 2169 | 89.2 | 582 | 22 AAB81987 | Ganglioside GD3 sp |
| 40 | 2168.5 | 89.2 | 442 | 24 ABB80113 | Deglycosylated hea |
| 41 | 2168.5 | 89.2 | 442 | 24 ABR39474 | Humanised anti-Abe |
| 42 | 2168.5 | 89.2 | 442 | 24 ABU08320 | Humanised antibody |
| 43 | 2164.5 | 89.0 | 459 | 14 AAR42066 | Human anti-HBs hea |
| 44 | 2161 | 88.9 | 464 | 23 ABG91842 | Human antibody fra |
| 45 | 2161 | 88.9 | 464 | 23 ABG78151 | Human Fv molecule |

ALIGNMENTS

RESULT 1
AAR33311
ID AAR33311 standard; Protein: 453 AA.
XX
AC AAR33311;
XX
DT 25-MAR-2003 (updated)
DT 05-JUL-1993 (first entry)
XX
DE Humanised MaE11 Version 1 (intact IgG) heavy chain.
XX
KW Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; Fab; humaellv1.
OS Synthetic.
XX
PN WO9304173-A1.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-US06860.
XX
PR 14-AUG-1991; 91US-0744768.
PR 07-MAY-1992; 92US-0879495.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1993-094004/11.
XX

| | |
|----|---|
| PT | Polyptide(s) binding to specific Fc epsilon receptors - act as |
| PT | IgE antagonists; useful for treating and preventing IgE-mediated disorders e.g. allergies |
| XX | |
| XX | Example 4; Fig 3; 113pp; English. |
| XX | |
| CC | Residues were selected from MaElI and inserted or substituted into |
| CC | a human Fab antibody background (Vh region Kabat subgroup III and V1 |
| CC | region kappa subgroup I). A first version, humaelivl or version 1 is |
| CC | cited below. The affinity of version 1 was assayed and found to be |
| CC | ca. 100 times lower than that of the donor antibody MaElI. |
| CC | Therefore, further modifications in the sequence of version 1 |
| CC | were made. |
| CC | (Updated on 25-MAR-2003 to correct PN field.) |
| XX | |
| SQ | Sequence 453 AA; |
| | Query Match 100.0%; Score 2432; DB 14; Length 453; |
| | Best Local Similarity 100.0%; Pred. No. 3.5e-144; |
| | Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSSTNY 60 |
| DB | 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSSTNY 60 |
| QY | 61 ADSVKGRFTISRDDSKNTFFYLQMSLRAEDTAVYYCARGSHYFGHWHFVAVWGQGTFLTVS 120 |
| DB | 61 ADSVKGRFTISRDDSKNTFFYLQMSLRAEDTAVYYCARGSHYFGHWHFVAVWGQGTFLTVS 120 |
| QY | 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPVL 180 |
| DB | 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPVL 180 |
| QY | 181 QSSGLYSLSSVTVPSSSLGTQTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240 |
| DB | 181 QSSGLYSLSSVTVPSSSLGTQTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240 |
| QY | 241 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAKTKPRE 300 |
| DB | 241 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAKTKPRE 300 |
| QY | 301 QYNSTRYRVSVLTVLHODWLNGREYKCCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360 |
| DB | 301 QYNSTRYRVSVLTVLHODWLNGREYKCCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360 |
| QY | 361 REEMTKNQVSLTCLVKGFYPFDIAVENESGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 420 |
| DB | 361 REEMTKNQVSLTCLVKGFYPFDIAVENESGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 420 |
| QY | 421 SRWQQGNVFSCSYMHEALHNHYTQKSLSLSPGK 453 |
| DB | 421 SRWQQGNVFSCSYMHEALHNHYTQKSLSLSPGK 453 |
| | |
| | RESULT 2 |
| AA | AA85199 |
| ID | AA85199 standard; protein; 453 AA. |
| XX | |
| AC | AA85199; |
| XX | |
| DT | 29-JUN-2000 (first entry) |
| XX | |
| DE | Heavy chain amino acid sequence of the humanised MaElI antibody. |
| XX | |
| KW | Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCBL; FCEH; |
| KW | low affinity binding receptor; high affinity binding receptor; allergy; |
| KW | diagnosis; treatment; histamine release; heavy chain; prevent; chimeric. |
| XX | |
| OS | Mus sp. |
| OS | Homo sapiens. |
| XX | |
| PN | US6037453-A. |
| XX | |

| | | | |
|--|----------|---|-----|
| Db | 421 | SRWQGNVFCSCVMHEALHNHYTKLSLSPGK | 453 |
| RESULT 3 | | | |
| AAW95659 | | | |
| ID | AAW95659 | standard; protein; 451 AA. | |
| XX | AC | AAW95659; | |
| XX | XX | 08-JUN-1999 (first entry) | |
| XX | XX | Mus musculus anti-IgE e25 full length variable heavy chain. | |
| XX | DE | | |
| XX | XX | Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; | |
| KW | KW | histamine; production; hypersensitivity; allergen; anaphylaxis; | |
| KW | KW | atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; | |
| KW | XX | eczema; anaphylactic shock; urticaria. | |
| XX | OS | Mus musculus. | |
| XX | XX | WO9901556-A2. | |
| XX | XX | 14-JAN-1999. | |
| XX | XX | 30-JUN-1998; 98WO-US13410. | |
| XX | XX | 02-JUL-1997; 97US-0887352. | |
| XX | XX | (GETH) GENENTECH INC. | |
| XX | XX | Jardieu PM, Lowe J, Lowman HB, Presta LG; | |
| XX | PI | WPI; 1999-106057/09. | |
| XX | DR | | |
| XX | XX | Improving affinity of polypeptides, particularly anti-IgE antibodies | |
| PT | PT | - by identifying aspartyl residues which undergo isomerisation and | |
| PT | PT | substituting alternative residues and screening for affinity against | |
| PT | PT | the target | |
| XX | XX | | |
| XX | PS | Disclosure; Pages 92-94; 129pp; English. | |
| XX | XX | | |
| XX | CC | The sequence is that of the full length heavy chain of e25. It | |
| CC | CC | was used as part of a method to improve the affinity of anti-IgE | |
| CC | CC | antibodies such as e26 and e27. The e26 and e27 antibodies can | |
| CC | CC | be used for reducing or preventing IgE mediated production of | |
| CC | CC | histamine in a mammal. They can be used for treating a disorder | |
| CC | CC | mediated by IgE such as hypersensitivity, atopic allergy, asthma, | |
| CC | CC | allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic | |
| CC | CC | shock and urticaria. The antibodies can also be used for affinity | |
| CC | CC | purification, detection and diagnosis. | |
| XX | XX | | |
| SQ | Sequence | 451 AA; | |
| Query Match | | | |
| Best Local Similarity 98.3%; Score 2391; DB 20; Length 451; | | | |
| Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1; | | | |
| QY | 1 | EVOLVESGGLVOPGSLRSCAVSGYSITSGYSWNWIRQAPGKLEWASITYDGSNTY | 60 |
| Db | 1 | EVOLVESGGLVOPGSLRSCAVSGYSITSGYSWNWIRQAPGKLEWASITYDGSNTY | 60 |
| QY | 61 | ADSVKGRFTISRDDSKNTFFLOMNSLRAEDTAVYVCARGSHYFCHWHFAVWGOGTLTVTS | 120 |
| Db | 61 | NPSVKGRFTISRDDSKNTFFLOMNSLRAEDTAVYVCARGSHYFCHWHFAVWGOGTLTVTS | 120 |
| QY | 121 | SASTKGGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL | 180 |
| Db | 121 | SAST--KGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL | 178 |
| QY | 181 | QSSGLYSLSSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHCTCPCPAPEL | 240 |
| Db | 179 | QSSGLYSLSSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHCTCPCPAPEL | 238 |
| Query Match | | | |
| Best Local Similarity 98.9%; Pred. No. 1.3e-141; | | | |
| Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1; | | | |
| QY | 241 | LGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE | 300 |
| Db | 239 | LGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE | 298 |
| QY | 301 | QYNSTRVRSVSLVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS | 360 |
| Db | 299 | QYNSTRVRSVSLVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS | 358 |
| QY | 361 | REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK | 420 |
| Db | 359 | REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK | 418 |
| QY | 421 | SRWQGNVFCSCVMHEALHNHYTKLSLSPGK | 453 |
| Db | 419 | SRWQGNVFCSCVMHEALHNHYTKLSLSPGK | 451 |
| RESULT 4 | | | |
| AAW95661 | | | |
| ID | AAW95661 | standard; protein; 451 AA. | |
| XX | AC | AAW95661; | |
| XX | XX | 08-JUN-1999 (first entry) | |
| XX | XX | Mus musculus anti-IgE e26 full length heavy chain. | |
| XX | XX | | |
| KW | KW | Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; | |
| KW | KW | histamine; production; hypersensitivity; allergen; anaphylaxis; | |
| KW | KW | atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; | |
| KW | XX | eczema; anaphylactic shock; urticaria. | |
| XX | OS | Mus musculus. | |
| XX | XX | WO9901556-A2. | |
| XX | XX | 14-JAN-1999. | |
| XX | XX | 30-JUN-1998; 98WO-US13410. | |
| XX | XX | 02-JUL-1997; 97US-0887352. | |
| XX | XX | (GETH) GENENTECH INC. | |
| XX | XX | Jardieu PM, Lowe J, Lowman HB, Presta LG; | |
| XX | PI | WPI; 1999-106057/09. | |
| XX | DR | | |
| XX | PT | Improving affinity of polypeptides, particularly anti-IgE antibodies | |
| PT | PT | - by identifying aspartyl residues which undergo isomerisation and | |
| PT | PT | substituting alternative residues and screening for affinity against | |
| PT | PT | the target | |
| XX | XX | | |
| XX | PS | Disclosure; Pages 95-96; 129pp; English. | |
| XX | XX | | |
| XX | CC | The sequence is that of the full length heavy chain of e26. It | |
| CC | CC | was used as part of a method to improve the affinity of anti-IgE | |
| CC | CC | antibodies such as e26 and e27. The e26 and e27 antibodies can | |
| CC | CC | be used for reducing or preventing IgE mediated production of | |
| CC | CC | histamine in a mammal. They can be used for treating a disorder | |
| CC | CC | mediated by IgE such as hypersensitivity, atopic allergy, asthma, | |
| CC | CC | allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic | |
| CC | CC | shock and urticaria. The antibodies can also be used for affinity | |
| CC | CC | purification, detection and diagnosis. | |
| XX | XX | | |
| SQ | Sequence | 451 AA; | |
| Query Match | | | |
| Best Local Similarity 98.3%; Score 2391; DB 20; Length 451; | | | |
| Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1; | | | |
| QY | 1 | EVOLVESGGLVOPGSLRSCAVSGYSITSGYSWNWIRQAPGKLEWASITYDGSNTY | 60 |
| Db | 1 | EVOLVESGGLVOPGSLRSCAVSGYSITSGYSWNWIRQAPGKLEWASITYDGSNTY | 60 |
| QY | 61 | ADSVKGRFTISRDDSKNTFFLOMNSLRAEDTAVYVCARGSHYFCHWHFAVWGOGTLTVTS | 120 |
| Db | 61 | NPSVKGRFTISRDDSKNTFFLOMNSLRAEDTAVYVCARGSHYFCHWHFAVWGOGTLTVTS | 120 |
| QY | 121 | SASTKGGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL | 180 |
| Db | 121 | SAST--KGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL | 178 |
| QY | 181 | QSSGLYSLSSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHCTCPCPAPEL | 240 |
| Db | 179 | QSSGLYSLSSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHCTCPCPAPEL | 238 |
| Query Match | | | |
| Best Local Similarity 98.9%; Pred. No. 1.3e-141; | | | |
| Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1; | | | |
| QY | 1 | EVOLVESGGLVOPGSLRSCAVSGYSITSGYSWNWIRQAPGKLEWASITYDGSNTY | 60 |
| Db | 1 | EVOLVESGGLVOPGSLRSCAVSGYSITSGYSWNWIRQAPGKLEWASITYDGSNTY | 60 |

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIRQAPGKLEWVASITYDGSNTY 60
 QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
 Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
 QY 121 SASTKGKPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
 Db 121 SAST--KGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
 QY 181 QSSGLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCPCPAPEL 240
 Db 179 QSSGLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCPCPAPEL 238
 QY 241 LGGPSVFLFPPKPKDLMISRTEPTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREE 300
 Db 239 LGGPSVFLFPPKPKDLMISRTEPTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREE 298
 QY 301 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIERTISKAKQPREPOVYTLPPS 360
 Db 299 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIERTISKAKQPREPOVYTLPPS 358
 QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 420
 Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 418
 QY 421 SRWQGNVFSCSVNHEALHNHYTKQSLSPGK 453
 Db 419 SRWQGNVFSCSVNHEALHNHYTKQSLSPGK 451

RESULT 5

AA85201
 ID AAY85201 standard; protein; 451 AA.

AC AAY85201;

DT 29-JUN-2000 (first entry)

DE Light chain amino acid sequence of anti-human IgE antibody.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcEL; FcHE; low affinity binding receptor; high affinity binding receptor; allergy; diagnosis; treatment; histamine release; heavy chain; prevent.

OS Mus sp.

XX US6037453-A.

XX 14-MAR-2000.

XX 06-JUN-1995; 9505-0466151.

XX 15-MAR-1995; 9505-0405617.

XX 14-AUG-1992; 92WO-US06860.

XX 26-JAN-1994; 94US-0185899.

XX (GETH) GENENTECH INC.

XX Presta LG, Jardieu PM;

XX WPI; 2000-269913/23.

XX New bispecific antibodies, useful for treating immunoglobulin E-mediated disease, binds to IgE, but only when on the low affinity receptor, and to an antigen other than IgE

PS Claim 15; Column 73-76; 48pp; English.

XX This sequence represents the light chain amino acid sequence of a mouse anti-human immunoglobulin E (IgE) antibody. The invention relates to a bispecific antibody that binds specifically to IgE when IgE is bound to its low affinity receptor (FcEL), but does not bind to IgE, when IgE is

CC bound to its high affinity receptor (FCEH). The bispecific antibody comprises an IgE-binding arm with human framework residues of a recipient human antibody and donor murine CDR (complementarity determining region) residues, but with at least one human CDR residue replacing the analogous murine residue. The antibody also comprises an Fv that is specific for a predetermined antigen other than IgE. The antibodies work by displacing bound IgE from its receptor, or via competitive inhibition of its binding. The bispecific antibodies are used for diagnosis, treatment and prevention of allergy and other IgE-mediated diseases, also, when immunobilised, for the isolation of FcEL from cells (for research or therapy). The bispecific antibodies of the invention do not cause granulation or release of histamine from mast cells.

XX Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 21; Length 451;
 Best Local Similarity 98.9%; Pred. No. 1.3e-141;

Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIRQAPGKLEWVASITYDGSNTY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIRQAPGKLEWVASITYDGSNTY 60

QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120

Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120

QY 121 SASTKGKPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCPCPAPEL 240

Db 179 QSSGLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDLMISRTEPTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREE 300

Db 239 LGGPSVFLFPPKPKDLMISRTEPTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREE 298

QY 301 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIERTISKAKQPREPOVYTLPPS 360

Db 299 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIERTISKAKQPREPOVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 420

Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 418

QY 421 SRWQGNVFSCSVNHEALHNHYTKQSLSPGK 453

Db 419 SRWQGNVFSCSVNHEALHNHYTKQSLSPGK 451

RESULT 6

AA847088

ID AAB47088 standard; protein; 451 AA.

XX AAB47088;

XX 08-MAY-2001 (first entry)

XX Anti-IgE antibody, E26, heavy chain.

XX Light chain; heavy chain; anti-IgE antibody; E26; transfection; green fluorescent protein; GFP; promoter; expression.

XX Chimeric - Homo sapiens.

XX Chimeric - Mus musculus.

XX WO200104306-A1..

XX 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US18841.

XX 12-JUL-1999; 99US-0143360.
XX (GETH) GENENTECH INC.
XX Chisholm V, Crowley CW, Krummen LA, Meng YG;
XX WPI; 2001-138352/14.
XX Novel polynucleotide construct for screening and obtaining cells
XX expressing high levels of desired protein, comprises amplifiable
XX selectable gene, fluorescent protein gene and sequence encoding desired
XX product
XX
XX Disclosure; Fig 13B; 75pp; English.
XX
XX The sequences given in AAB47087-88 represent the light and heavy
XX chains of the anti-IgE antibody, E26. These sequences were expressed
XX by the construct of the invention, which comprises an amplifiable
XX selectable gene, a green fluorescent protein gene (GFP), and a
XX selected sequence encoding a desired product, which is operably
XX linked to either the amplifiable selectable gene or to the GFP gene,
XX and to a promoter. Constructs such as this, are useful for producing
XX a desired product by introduction into a suitable eukaryotic cell,
XX culturing the resultant eukaryotic cell under conditions so as to
XX express the desired product, and recovering the desired product from
XX the culture medium. The constructs are efficient for identifying and
XX selecting for stable eukaryotic cells expressing high levels of a
XX desired product. They are suitable for earlier and faster screening
XX of transfected cells.
XX
XX Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 22; Length 451;
Best Local Similarity 98.9%; Pred. No. 1.3e-141;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWASITYDGSNTY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
QY 121 SASTKKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVL 180
Db 121 SAST--KGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 238
QY 241 LGGPSVFLPPKPKDFTLMSIRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATTPREE 300
Db 239 LGGPSVFLPPKPKDFTLMSIRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATTPREE 298
QY 301 QYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRMQQGNVSCSVNHEALNHYTKQSLSPGK 453
Db 419 SRMQQGNVSCSVNHEALNHYTKQSLSPGK 451

RESULT 7
AAB76948
ID AAB76948 standard; Protein; 451 AA.

XX AAB76948;
XX 17-APR-2001 (first entry)
XX Full length heavy chain sequence of e25 SEQ ID 14.
XX
XX Antibody: antiasthmatic; antiallergic; ophthalmological; dermatological;
XX antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
XX conjunctivitis; eczema; urticaria; food allergy.
XX Synthetic.
XX US6172213-B1.
XX PN 09-JAN-2001.
XX PD
XX PF 30-JUN-1998; 98US-0109207.
XX PR
XX PR 02-JUL-1997; 97US-0051554.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX WPI; 2001-122353/13.
XX
XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX properties, produced by substituting aspartyl residues in unimproved
XX immunoglobulin E prone to isomerization by other residues by affinity
XX maturation with phage display
XX
XX Disclosure; Fig 12; 87pp; English.
XX
XX This invention relates to a nucleotide sequence encoding an antibody
XX with improved anti-IgE antibody activity. The antibody has improved
XX action due to a process comprising, a) identifying aspartyl residues
XX prone to isomerisation in unimproved anti-IgE (immunoglobulin E)
XX antibody; b) substituting alternative residues to create candidate
XX molecules, and c) selecting those candidate molecules which display
XX affinity against the target molecule. Use of the antibody results in
XX antiasthmatic; antiallergic; ophthalmological; dermatological and
XX antiinflammatory activity. The antibodies are useful for treating
XX IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
XX eczema, urticaria and food allergies. The mutant antibodies produced by
XX the above mentioned nucleic acids may also be used as affinity
XX purification agents and in diagnostic assays for detecting the expression
XX of an antigen of interest in specific cell, tissues or serum. Amino acid
XX sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of
XX the invention. Polynucleotide sequence AAF69253 represents an expression
XX plasmid used in the course of the invention, and oligonucleotides
XX AAF69254 - AAF69271 are used in the generation of affinity improved
XX anti-IgE antibodies.
XX
XX Sequence 451-AA;
SQ
Query Match 98.3%; Score 2391; DB 22; Length 451;
Best Local Similarity 98.9%; Pred. No. 1.3e-141;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWASITYDGSNTY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
QY 121 SASTKKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVL 180
Db 121 SAST--KGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 240
XX

Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTCCPCPAPEL 238
 QY 241 LGGPSVFLPPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREE 300
 Db 239 LGGPSVFLPPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREE 298
 QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
 Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
 QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
 Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
 QY 421 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
 Db 419 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
 RESULT 8
 AAB76950
 ID AAB76950 standard; Protein; 451 AA.
 XX
 AC AAB76950;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE Full length heavy chain sequence of e26 SEQ ID 16.
 XX
 KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 XX
 OS Synthetic.
 XX
 US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-0109207.
 XX
 PR 02-JUL-1997; 97US-0051554.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2001-122353/13.
 XX
 PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phage display
 XX
 PS Claim 2; Fig 12; 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody
 CC with improved anti-IgE antibody activity. The antibody has improved
 CC action due to a process comprising, a) identifying aspartyl residues
 CC prone to isomerisation in unimproved anti-IgE (immunoglobulin E)
 CC antibody; b) substituting alternative residues to create candidate
 CC molecules, and c) selecting those candidate molecules which display
 CC affinity against the target molecule. Use of the antibody results in
 CC antiasthmatic; antiallergic; ophthalmological; dermatological and
 CC antiinflammatory activity. The antibodies are useful for treating
 CC IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
 CC eczema, urticaria and food allergies. The mutant antibodies produced by
 CC the above mentioned nucleic acids may also be used as affinity
 CC purification agents and in diagnostic assays for detecting the expression
 CC of an antigen of interest in specific cell, tissues or serum. Amino acid
 CC sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of
 CC the invention. Polynucleotide sequence AAB769253 represents an expression

CC plasmid used in the course of the invention, and oligonucleotides
 CC AAF69254 - AAF69271 are used in the generation of affinity improved
 CC anti-IgE antibodies.
 XX
 SQ Sequence 451 AA;
 Query Match 98.3%; Score 2391; DB 22; Length 451;
 Best Local Similarity 98.9%; Pred. No. 1.3e-141;
 Matches 448; Conservative 0; Mismatches 3; Indels 2; Caps 1;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWNIRQAPCKGLEWVASIYDGSTNY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWNIRQAPCKGLEWVASIYDGSTNY 60
 QY 61 ADSVKRGRTISRDDSKNTFFLOMNSLRADETAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
 Db 61 NPSVKGRITISRDDSKNTFFLOMNSLRADETAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
 QY 121 SASTKGKPSVFLPAPSSKTSSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
 Db 121 SAST--KGPSVFLPAPSSKTSSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
 QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTCCPCPAPEL 240
 Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTCCPCPAPEL 238
 QY 241 LGGPSVFLPPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREE 300
 Db 239 LGGPSVFLPPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREE 298
 QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
 Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
 QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
 Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
 QY 421 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
 Db 419 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
 RESULT 9
 AAY50031
 ID AAY50031 standard; protein; 451 AA.
 XX
 AC AAY50031;
 XX
 DT 19-JAN-2000 (first entry)
 XX
 DE Human E27 anti-IgE antibody heavy chain.
 XX
 KW Immunoglobulin E; IgE; antibody; vascular endothelial growth factor;
 KW VEGF; chimeric; IgG; assay; Fc gamma receptor; low affinity; hexamer;
 KW complex; cross-linked; enzyme-linked immunosorbent assay; ELISA;
 KW heavy chain.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO9951642-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US06858.
 XX
 PR 02-APR-1998; 98US-0054255.
 PR 15-JAN-1999; 99US-0116100.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Idusogie EE, Mulkerin MG, Presta LG, Shields RL;

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XX WPI; 1999-620197/53.
XX
XX Antibody variants useful in receptor binding assays and in therapy of
XX conditions needing treatment
XX
XX Example 1; Fig 4B; 69pp; English.
XX
XX This sequence represents human E27 anti-IgE (immunoglobulin E) antibody
XX heavy chain, which, along with the E27 light chain (AAV50030), comprises
XX the E27 anti-IgE antibody. The E27 antibody binds the constant regions
XX of IgE, and when mixed with IgE in an equimolar ratio, forms a stable
XX hexamer consisting of three E27 molecules and 3 IgE molecules. This
XX complex-forming ability can be utilised in an assay for the binding of
XX IgG to FC gamma receptors FC-gamma-1IIa, FC-gamma-1Ib and FC-gamma-1II,
XX which have IgG affinities in the micromolar range and so cannot be
XX assayed via a standard ELISA (enzyme-linked immunosorbent assay)
XX protocol. The low affinity receptor binding assay uses E27 and a
XX recombinant chimeric form of IgE, consisting of a human IgE FC region
XX and the Fab regions of an anti-VEGF (vascular endothelial growth factor)
XX antibody, which binds two VEGF molecules per mole of anti-VEGF chimeric
XX IgE. When recombinant human VEGF is added at at 2:1 molar ratio to the
XX IgE:E27 hexamer complexes, the hexamers are linked into larger complexes
XX via IgE Fab:VEGF interactions. The E27 component of this complex binds
XX to the FC-gamma-1Ib, FC-gamma-1Ib and FC-gamma-1II alpha subunits to
XX permit detection via ELISA.
XX
XX Sequence 451 AA;
XX
XX Query Match 97.4%; Score 2369; DB 20; Length 451;
XX Best Local Similarity 98.0%; Pred. No. 3e-140;
XX Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
XX
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIKYSGETKY 60
Qy 61 ADSVKGRFTISRDDSKNTFFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
Qy 121 SASTKKGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSWVTPVSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCCPCPAPEL 240
Db 179 QSSGLYSLSWVTPVSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCCPCPAPEL 238
Qy 241 LGGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
Db 239 LGGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
Qy 301 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 360
Db 299 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 358
Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 418
Qy 421 SRVQOGNVCFSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRVQOGNVCFSVMHEALHNHYTQKSLSLSPGK 451

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RESULT 10

AAW95663

ID AAW95663 standard; protein: 451 AA.

XX

AC AAW95663;

XX

DT 08-JUN-1999 (first entry)

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XX Mus musculus anti-IgE e27 full length heavy chain.
XX
XX Heavy chain: IgE; antibody: anti-IgE; reduction: prevention;
XX histamine; production; hypersensitivity; allergen; anaphylaxis;
XX atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
XX eczema; anaphylactic shock; urticaria.
XX
XX Mus musculus.
XX
XX WO9901556-A2.
XX
XX 14-JAN-1999.
XX
XX 30-JUN-1998; 98WO-US13410.
XX
XX 02-JUL-1997; 97US-0887352.
XX
XX (GETH ) GENENTECH INC.
XX
XX Jardieu PM, Lowe J, Lowman HB, Presta LG;
XX
XX WPI; 1999-106057/09.
XX
XX Improving affinity of polypeptides, particularly anti-IgE antibodies
XX - by identifying aspartyl residues which undergo isomerisation and
XX substituting alternative residues and screening for affinity against
XX the target
XX
XX Disclosure; pages 97-99; 129pp; English.
XX
XX The sequence is that of the full length heavy chain of e27. It
XX was used as part of a method to improve the affinity of anti-IgE
XX antibodies such as e26 and e27. The e26 and e27 antibodies can
XX be used for reducing or preventing IgE mediated production of
XX histamine in a mammal. They can be used for treating a disorder
XX mediated by IgE such as hypersensitivity, atopic allergy, asthma,
XX allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic
XX shock and urticaria. The antibodies can also be used for affinity
XX purification, detection and diagnosis.
XX
XX Sequence 451 AA;
XX
XX Query Match 97.4%; Score 2369; DB 20; Length 451;
XX Best Local Similarity 98.0%; Pred. No. 3e-140;
XX Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
XX
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIKYSGETKY 60
Qy 61 ADSVKGRFTISRDDSKNTFFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
Qy 121 SASTKKGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSWVTPVSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCCPCPAPEL 240
Db 179 QSSGLYSLSWVTPVSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCCPCPAPEL 238
Qy 241 LGGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
Db 239 LGGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
Qy 301 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 360
Db 299 QYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 358
Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420

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Db 359 REEMTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTPPVLDSDGSFFLXSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 451

RESULT 11
AAB07473
ID AAB07473 standard; protein; 451 AA.
XX AAB07473;
AC AAB07473;
DT 20-OCT-2000 (first entry)
XX
XX Amino acid sequence of E27 and anti-IgE antibody heavy chain.
DE anti-IgE antibody; heavy chain; Fc region; effector function; cancer;
XX allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
KW
KW
XX
OS Synthetic.
XX
XX WO200042072-A2.
PN
XX
XX 20-JUL-2000.
XX
XX 14-JAN-2000; 2000WO-US00973.
XX
XX 15-JAN-1999; 99US-0116023.
XX (GETH) GENENTECH INC.
FA
XX
XX Presta LG;
PI
XX
XX WPI; 2000-476035/41.
DR
XX
XX New Fc region-containing polypeptides that have altered effector
PT function due to one or more amino acid modifications in the Fc region,
PT useful in the treatment of cancer and allergic conditions such as
PT asthma
XX
XX Disclosure; Fig 4B; 132pp; English.
PS
XX
XX The present sequence represents the E27 and anti-IgE antibody heavy
CC chain. The protein is used to produce Fc region-containing polypeptides
CC that have altered effector function as a consequence of one or more
CC amino acid modifications in the Fc region. The variant polypeptides are
CC useful for treating cancer, allergic conditions such as asthma (with an
CC anti-IgE antibody), and LFA-1-mediated disorders. Where the polypeptide
CC binds the HER2 receptor, the disorder preferably is HER2-expressing
CC cancer, e.g. a benign or malignant tumour characterized by overexpression
CC of the HER2 receptor. Such cancers include breast cancer, squamous cell
CC cancer, small-cell lung cancer, non-small cell lung cancer,
CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
CC cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer,
CC colorectal cancer, endometrial carcinoma, salivary gland carcinoma,
CC kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid
CC cancer, hepatic carcinoma and various types of head and neck cancer.
XX
XX Sequence 451 AA;
SQ

Query Match 97.4%; Score 2369; DB 21; Length 451;
Best Local Similarity 98.0%; Pred. No. 3e-140;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps. 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNIROAPGKLEWVASIYDGTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNIROAPGKLEWVASIRYGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFFLQNNLSRAEDTAVYICARGSHYFGHWFVWGQGTITVTS 120
Db 61 NPSVKGRITISRDDSKNTFFLQNNLSRAEDTAVYICARGSHYFGHWFVWGQGTITVTS 120

QY 121 SASTKKGSPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGSPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVLDHDLNGLNKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLDHDLNGLNKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTPPVLDSDGSFFLXSKLTVDK 420.
Db 359 REEMTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTPPVLDSDGSFFLXSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 451

RESULT 12
AAB74212
ID AAB74212 standard; protein; 451 AA.
XX AAB74212;
AC AAB74212;
DT 17-MAY-2001 (first entry)
XX
XX E27 anti-IgE antibody heavy chain.
DE
XX
XX Antibody; antigen; cancer; allergy; asthma; LFA-mediated;
KW autoImmune; vasculitis.
XX
XX Unidentified.
OS
XX US6194551-B1.
PN
XX 27-FEB-2001.
PD
XX 31-MAR-1999; 99US-0282505.
XX
XX 02-APR-1998; 98US-0080447.
PR
XX (GETH) GENENTECH INC.
PI
XX Idusogie EE, Presta LG, Mulkerrin MG;
XX WPI; 2001-217935/22.
XX
XX Novel polypeptide variant useful for treating cancers, allergic
PT diseases such as asthma and autoimmune diseases, comprises human
PT immunoglobulin-G Fc region, retains the ability to bind antigen and
PT does not activate complement
XX
XX Disclosure; Fig 4; 30pp; English.
PS
XX The present invention relates to a variant of an antibody
CC having a human immunoglobulin (Ig)G Fc region, with an
CC amino acid substitution. The mutant retains the ability to
CC bind antigen. The invention is useful for determining the
CC presence of a protein of interest, by exposing the sample
CC suspected of containing the protein to the antibody and
CC determining the binding of it to the sample. The antibody
CC is also useful for treating cancer, allergic conditions
CC including asthma, LFA-mediated disorders, autoimmune
CC disorders and vasculitis.
XX
XX Sequence 451 AA;
SQ

| | | |
|---------------------------|--|----------------------------|
| PS | Claim 4; Fig 12; 87pp; English. | |
| XX | This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgE antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgE antibodies. | |
| SQ | Sequence 451 AA; | |
| Query Match | 97.4%; Score 2369; DB 22; Length 451; | |
| Best Local Similarity | 98.0%; Pred. No. 3e-140; | |
| Matches 444; Conservative | 0; Mismatches 7; Indels 2; Gaps 1; | |
| QY | 1 EVOLVESGGLVOPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS | TNY 60 |
| Db | 1 EVOLVESGGLVOPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSETKY | 60 |
| QY | 61 ADSVKGRFTISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTV | TVS 120 |
| Db | 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTV | TVS 120 |
| QY | 121 SASTKKGPSVFLPAPSSKSTGGTAALGCLVKDYFPEPTVYSWNSGALTS | GVHFFPAVL 180 |
| Db | 121 SAST--KGPSVFLPAPSSKSTGGTAALGCLVKDYFPEPTVYSWNSGALTS | GVHFFPAVL 178 |
| QY | 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPCAP | E 240 |
| Db | 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPCAP | E 238 |
| QY | 241 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN | AKTKPREE 300 |
| Db | 239 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN | AKTKPREE 298 |
| QY | 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE | POVYTLPPS 360 |
| Db | 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE | POVYTLPPS 358 |
| QY | 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF | FLYSLKLTVDK 420 |
| Db | 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF | FLYSLKLTVDK 418 |
| QY | 421 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK | 453 |
| Db | 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK | 451 |
| RESULT 13 | | |
| AAB76952 | | |
| ID | AAB76952 | standard; Protein; 451 AA. |
| XX | | |
| AC | AAB76952; | |
| XX | | |
| DT | 17-APR-2001 | (first entry) |
| XX | | |
| DE | Full length heavy chain sequence of e27 SEQ ID 18. | |
| XX | | |
| KW | Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; | |
| KW | antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; | |
| KW | conjunctivitis; eczema; urticaria; food allergy. | |
| XX | | |
| OS | Synthetic. | |
| XX | | |
| PN | US6172213-B1. | |
| XX | | |
| PD | 09-JAN-2001. | |
| XX | | |
| PF | 30-JUN-1998; | 98US-0109207. |
| XX | | |
| PR | 02-JUL-1997; | 97US-0051554. |
| XX | | |
| PA | (GETH) GENENTECH INC. | |
| XX | | |
| PI | Lowman HB, Presta LG, Jardieu PM, Lowe J; | |
| XX | | |
| DR | WPI; 2001-122353/13. | |
| XX | | |
| PT | New nucleic acid encoding anti-immunoglobulin E antibody with improved | |
| PT | properties, produced by substituting aspartyl residues in unimproved | |
| PT | immunoglobulin E prone to isomerization by other residues by affinity | |
| PT | maturation with phage display | |
| XX | | |

fusion protein.
 Synthetic.
 WO9937779-A1.
 29-JUL-1999.
 19-JAN-1999; 99WO-US01081.
 24-JUL-1998; 98US-0122513.
 22-JAN-1998; 98US-0012116.
 20-FEB-1998; 98WO-US03337.
 24-JUL-1998; 98US-0121952.
 (GETH) GENENTECH INC.
 Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;
 Zapata GA;
 WPI; 1999-469134/39.
 New conjugates of nonproteinaceous polymers with antibody fragments,
 used for treating inflammatory disorders
 Disclosure; Page 354-355; 360pp; English.
 The present invention describes a novel conjugate having one or more
 antibody fragments covalently attached to one or more nonproteinaceous
 polymer molecules, where the apparent size of the conjugate is at least
 about 500 kDa. Conjugates of antibody fragments which bind the human
 interleukin (IL) 8 with a nonproteinaceous polymer can be used for
 treating inflammatory disorders e.g. acute lung injury, ischaemic
 reperfusion disorder, and autoimmune diseases. They can also be used
 for treating e.g. inflammatory skin diseases including psoriasis and
 atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
 diseases. The conjugates can also be used as reagents in an animal
 model system for in vivo study of the biological functions of the
 antigen recognised by the conjugate. The present sequence represents
 a recombinant immunoglobulin protein from the present invention.
 Query Match 91.1%; Score 2214.5; DB 20; Length 452;
 Best Local Similarity 92.7%; Pred. No. 1.4e-130;
 Matches 422; Conservative 8; Mismatches 20; Indels 5; Gaps 4;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSTISGYSNWNIRQAPCKGLEWVASI-TYDGSN 59
 DB 1 EVOLVSGGGGLVQPGGSLRLSCAASGYSTISGYSNWNIRQAPCKGLEWVGYIDPSNGETT 59
 QY 60 YADSVKGRFTISRDDSKNTFYLOMNSLRRAEDTAVYYCARGSH-YFGHWHFAVWGQGLTVT 118
 DB 60 YNQKFKGRFTLSRDNSKNTAYLQMNSLRRAEDTAVYYCARGDTRYNGDFFVWGQGLTVT 119
 QY 119 VSSASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFA 178
 DB 120 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFA 177
 QY 179 VLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHTCTPCPAP 238
 DB 178 VLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHTCTPCPAP 237
 QY 239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPR 298
 DB 238 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPR 297
 QY 299 EQYNSTYRVSVLTVHLHODLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 358
 DB 298 EQYNSTYRVSVLTVHLHODLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 357
 QY 359 PSREEMTKNOVSLTCLVKGYFSDTAWEHESGQPNENYKTTTPVLDSDGSFFLYSKLTV 418
 fusion protein.
 Synthetic.
 WO9937779-A1.
 29-JUL-1999.
 19-JAN-1999; 99WO-US01081.
 24-JUL-1998; 98US-0122513.
 22-JAN-1998; 98US-0012116.
 20-FEB-1998; 98WO-US03337.
 24-JUL-1998; 98US-0121952.
 (GETH) GENENTECH INC.
 Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;
 Zapata GA;
 WPI; 1999-469134/39.
 New conjugates of nonproteinaceous polymers with antibody fragments,
 used for treating inflammatory disorders
 Disclosure; Page 354-355; 360pp; English.
 The present invention describes a novel conjugate having one or more
 antibody fragments covalently attached to one or more nonproteinaceous
 polymer molecules, where the apparent size of the conjugate is at least
 about 500 kDa. Conjugates of antibody fragments which bind the human
 interleukin (IL) 8 with a nonproteinaceous polymer can be used for
 treating inflammatory disorders e.g. acute lung injury, ischaemic
 reperfusion disorder, and autoimmune diseases. They can also be used
 for treating e.g. inflammatory skin diseases including psoriasis and
 atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
 diseases. The conjugates can also be used as reagents in an animal
 model system for in vivo study of the biological functions of the
 antigen recognised by the conjugate. The present sequence represents
 a recombinant immunoglobulin protein from the present invention.
 Query Match 91.1%; Score 2214.5; DB 20; Length 452;
 Best Local Similarity 92.7%; Pred. No. 1.4e-130;
 Matches 422; Conservative 8; Mismatches 20; Indels 5; Gaps 4;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSTISGYSNWNIRQAPCKGLEWVASI-TYDGSN 59
 DB 1 EVOLVSGGGGLVQPGGSLRLSCAASGYSTISGYSNWNIRQAPCKGLEWVGYIDPSNGETT 59
 QY 60 YADSVKGRFTISRDDSKNTFYLOMNSLRRAEDTAVYYCARGSH-YFGHWHFAVWGQGLTVT 118
 DB 60 YNQKFKGRFTLSRDNSKNTAYLQMNSLRRAEDTAVYYCARGDTRYNGDFFVWGQGLTVT 119
 QY 119 VSSASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFA 178
 DB 120 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFA 177
 QY 179 VLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHTCTPCPAP 238
 DB 178 VLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHTCTPCPAP 237

Db 358 PSREEMTKNOVSLTCLVKGYFSDTAWEHESGQPNENYKTTTPVLDSDGSFFLYSKLTV 417
 QY 419 DKSRWQGNVFCVSMHEALHNHYTKSLSPGK 453
 Db 418 DKSRWQGNVFCVSMHEALHNHYTKSLSPGK 452
 RESULT 15
 AAB30322
 ID AAB30322 standard; Protein; 452 AA.
 XX
 AC AAB30322;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE Humanised anti-IL-8 antibody related protein SEQ ID NO: 71.
 XX
 KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
 KW adult respiratory distress syndrome; multiple organ failure;
 KW bacterial pneumonia; inflammatory bowel disease.
 XX
 OS Unidentified.
 XX
 PN US6133426-A.
 XX
 PD 17-OCT-2000.
 XX
 PF 20-FEB-1998; 98US-0026985.
 XX
 PR 21-FEB-1997; 97US-0038664.
 PR 22-JAN-1998; 98US-0074330.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Presta LG, Leong SR, Gonzalez TN;
 DR WPI; 2000-686027/67.
 XX
 DR Humanized anti-interleukin 8 monoclonal antibody variant useful for
 PT treating inflammatory disorders, such as adult respiratory distress
 PT syndrome, hypovolemic shock and ulcerative colitis -
 XX
 PS Disclosure; Column 199-202; 240pp; English.
 XX
 CC The present invention provides a number of humanised monoclonal anti-IL-8
 CC antibodies which can be used in the diagnosis and treatment of
 CC inflammatory disorders, including adult respiratory distress syndrome,
 CC septic shock, multiple organ failure, bacterial pneumonia and
 CC inflammatory bowel disease. The present sequence comprises one of the
 CC antibodies of the invention.
 XX
 SQ Sequence 452 AA;
 Query Match 91.1%; Score 2214.5; DB 21; Length 452;
 Best Local Similarity 92.7%; Pred. No. 1.4e-130;
 Matches 422; Conservative 8; Mismatches 20; Indels 5; Gaps 4;
 QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSTISGYSNWNIRQAPCKGLEWVASI-TYDGSN 59
 DB 1 EVOLVSGGGGLVQPGGSLRLSCAASGYSTISGYSNWNIRQAPCKGLEWVGYIDPSNGETT 59
 QY 60 YADSVKGRFTISRDDSKNTFYLOMNSLRRAEDTAVYYCARGSH-YFGHWHFAVWGQGLTVT 118
 DB 60 YNQKFKGRFTLSRDNSKNTAYLQMNSLRRAEDTAVYYCARGDTRYNGDFFVWGQGLTVT 119
 QY 119 VSSASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFA 178
 DB 120 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFA 177
 QY 179 VLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHTCTPCPAP 238
 DB 178 VLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHTCTPCPAP 237

| | | | |
|----|-----|---|-----|
| Qy | 239 | ELGGPSVFLPPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR | 298 |
| Db | 238 | ELGGPSVFLPPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR | 297 |
| Qy | 299 | EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL | 358 |
| Db | 298 | EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL | 357 |
| Qy | 359 | PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT | 418 |
| Db | 358 | PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT | 417 |
| Qy | 419 | DKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK | 453 |
| Db | 418 | DKSRWQOGNPFSCSVMEALHNHYTQKSLSLSPGK | 452 |

Search completed: August 12, 2003, 16:30:04
Job time : 56.3338 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:28:52 ; Search time 19.5782 seconds
(without alignments)
978.986 Million cell updates/sec

Title: US-09-802-077-8

Perfect score: 2432

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHHYTKSLSPGK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 2432 | 100.0 | 453 | 3 | US-08-466-151-8 |
| 2 | 2432 | 100.0 | 453 | 4 | US-08-466-163B-8 |
| 3 | 2391 | 98.3 | 451 | 2 | US-08-887-352B-14 |
| 4 | 2391 | 98.3 | 451 | 2 | US-08-887-352B-16 |
| 5 | 2391 | 98.3 | 451 | 3 | US-08-466-151-65 |
| 6 | 2391 | 98.3 | 451 | 3 | US-09-109-207C-14 |
| 7 | 2391 | 98.3 | 451 | 3 | US-09-109-207C-16 |
| 8 | 2391 | 98.3 | 451 | 3 | US-09-296-005-14 |
| 9 | 2391 | 98.3 | 451 | 3 | US-09-296-005-16 |
| 10 | 2369 | 97.4 | 451 | 2 | US-08-887-352B-18 |
| 11 | 2369 | 97.4 | 451 | 3 | US-09-109-207C-18 |
| 12 | 2369 | 97.4 | 451 | 3 | US-09-282-505-2 |
| 13 | 2369 | 97.4 | 451 | 3 | US-09-054-255-2 |
| 14 | 2369 | 97.4 | 451 | 3 | US-09-296-005-18 |
| 15 | 2369 | 97.4 | 451 | 4 | US-09-282-846-2 |
| 16 | 2369 | 97.4 | 451 | 4 | US-09-680-145-2 |
| 17 | 2214.5 | 91.1 | 452 | 3 | US-09-027-449-71 |
| 18 | 2214.5 | 91.1 | 452 | 3 | US-09-026-985-71 |
| 19 | 2214.5 | 91.1 | 452 | 4 | US-09-121-952A-71 |
| 20 | 2214.5 | 91.1 | 452 | 4 | US-09-234-340A-71 |
| 21 | 2179.5 | 89.6 | 449 | 4 | US-09-679-397-2 |
| 22 | 2179.5 | 89.6 | 449 | 4 | US-09-680-148-2 |
| 23 | 2179.5 | 89.6 | 449 | 4 | US-09-304-465A-2 |
| 24 | 2164.5 | 89.0 | 459 | 1 | US-08-157-101A-7 |
| 25 | 2132 | 87.7 | 478 | 3 | US-08-487-550-8 |
| 26 | 2132 | 87.7 | 478 | 4 | US-09-526-098-8 |
| 27 | 2117.5 | 87.1 | 473 | 3 | US-09-049-672A-4 |

Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 8, Appl
Sequence 7, Appl
Sequence 67, Appl
Sequence 4, Appl
Sequence 90, Appl
Sequence 8, Appl
Sequence 27, Appl
Sequence 81, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 10, Appl
Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid

TOPOLOGY: Linear
US-08-466-151-8

Query Match 100.0%; Score 2432; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASITYDGSNTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
DB 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
QY 121 SASTKKGVSFVPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 180
DB 121 SASTKKGVSFVPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 180
QY 181 QSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKHTCCPPCPAPEL 240
DB 181 QSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKHTCCPPCPAPEL 240
QY 241 LGGPSVFLPPPKDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 241 LGGPSVFLPPPKDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVTLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
DB 301 QYNSTYRVVSVLTVTLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
QY 361 REEMTNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
DB 361 REEMTNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQGNVSCSVNMHEALHNHYTKQSLSPGK 453
DB 421 SRWQGNVSCSVNMHEALHNHYTKQSLSPGK 453

RESULT 2

US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; PRIORITY FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-08-466-163B-8

Query Match 100.0%; Score 2432; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASITYDGSNTY 60

DB 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
DB 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQTLTVTS 120
QY 121 SASTKKGVSFVPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 180
DB 121 SASTKKGVSFVPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 180
QY 181 QSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKHTCCPPCPAPEL 240
DB 181 QSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKHTCCPPCPAPEL 240
QY 241 LGGPSVFLPPPKDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 241 LGGPSVFLPPPKDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVTLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
DB 301 QYNSTYRVVSVLTVTLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
QY 361 REEMTNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
DB 361 REEMTNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQGNVSCSVNMHEALHNHYTKQSLSPGK 453
DB 421 SRWQGNVSCSVNMHEALHNHYTKQSLSPGK 453

RESULT 3

US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-14

Query Match 98.3%; Score 2391; DB 2; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;

| | Matches | 448; | Conservative | 0; | Mismatches | 3; | Indels | 2; | Gaps | 1; |
|----|---------|--|--------------|----|------------|----|--------|----|------|----|
| QY | 1 | EVOLVESGGGLVQPGGSLURLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS | 60 | | | | | | | |
| Db | 1 | EVOLVESGGGLVQPGGSLURLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS | 60 | | | | | | | |
| QY | 61 | ADSVKGRRTTISRDDSKNTFYIQMNSLRADETAVYVCARGSHYFGCHWFAVWGQGLTVTS | 120 | | | | | | | |
| Db | 61 | NPSVAGRRTISRDDSKNTFYIQMNSLRADETAVYVCARGSHYFGCHWFAVWGQGLTVTS | 120 | | | | | | | |
| QY | 121 | SASTKKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL | 180 | | | | | | | |
| Db | 121 | SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL | 178 | | | | | | | |
| QY | 181 | QSSGLYLSLSSVTVPPSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL | 240 | | | | | | | |
| Db | 179 | QSSGLYLSLSSVTVPPSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL | 238 | | | | | | | |
| QY | 241 | LGGSVFLFPKPKDITLMSRTPETCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREE | 300 | | | | | | | |
| Db | 239 | LGGSVFLFPKPKDITLMSRTPETCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREE | 298 | | | | | | | |
| QY | 301 | QYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSKNALPAPIEKTISAKAGQPREPQVYITLPPS | 360 | | | | | | | |
| Db | 299 | QYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSKNALPAPIEKTISAKAGQPREPQVYITLPPS | 358 | | | | | | | |
| QY | 361 | REEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLVNDK | 420 | | | | | | | |
| Db | 359 | REEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLVNDK | 418 | | | | | | | |
| QY | 421 | SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK | 453 | | | | | | | |
| Db | 419 | SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK | 451 | | | | | | | |

RESULT 4
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-16

| | | | | |
|-----------------------|----------------|--------------------|----------|------------|
| Query Match | 98.3% | Score 2391 | DB 2 | Length 451 |
| Best Local Similarity | 98.9% | Pred. No. 3.9e-181 | | |
| Matches 448 | Conservative 0 | Mismatches 3 | Indels 2 | Gaps 1 |

| | | | | |
|----|-----|--|----------|-----|
| QY | 1 | EVOLVESGGGLVOPGGSRLRSLSCAVSGYSITSGYSNWIRQAPCKGLEWVASIITYDGS | TNY | 60 |
| DB | 1 | EVOLVESGGGLVOPGGSRLRSLSCAVSGYSITSGYSNWIRQAPCKGLEWVASIITYDGS | TNY | 60 |
| QY | 61 | ADSVKGRFTISRDDSKNTFYLOMNSLRAEDTAVVYICARGSHYEGHWHFAVMGQGLTVTS | | 120 |
| DB | 61 | NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVVYICARGSHYEGHWHFAVMGQGLTVTS | | 120 |
| QY | 121 | SASTKCKGSPVFLAPSSKSTSGGTAALGCLVXDYPPEVTVVSNWNSCALTS | GVHTFP | 180 |
| DB | 121 | SAST--KGPSVFLAPSSKSTSGGTAALGCLVXDYPPEVTVVSNWNSCALTS | GVHTFP | 178 |
| QY | 181 | QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPP | CAPEL | 240 |
| DB | 179 | QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPP | CAPEL | 238 |
| QY | 241 | LGSPSVFLPPPKPKDLMISRTPDEVTCVVVDVSHEDPEVKFNNYVDGVEVHN | AKTKPRE | 300 |
| DB | 239 | LGSPSVFLPPPKPKDLMISRTPDEVTCVVVDVSHEDPEVKFNNYVDGVEVHN | AKTKPRE | 298 |
| QY | 301 | QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI | ISKAKGP | 360 |
| DB | 299 | QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI | ISKAKGP | 358 |
| QY | 361 | REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT | PPVLDSDG | 420 |
| DB | 359 | REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT | PPVLDSDG | 418 |
| QY | 421 | SRWQGNVFSCSYMHHEALHNHYTQKSLSLSPGK | | 453 |
| DB | 419 | SRWQGNVFSCSYMHHEALHNHYTQKSLSLSPGK | | 451 |

RESULT 5

US-08-466-151-65

Sequence 65, Application US/08466151

Patent No. 6037453

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,151

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/466163

FILING DATE: 06-Jun-1995

APPLICATION NUMBER: 08/405617

FILING DATE: 15-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/185899

FILING DATE: 26-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/879495

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; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match      98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
QY 61 ADSVKGREITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 238
QY 241 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 6
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-16

Query Match      98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
QY 61 ADSVKGREITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 238
QY 241 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 7
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-16

Query Match      98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
QY 61 ADSVKGREITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 238
QY 241 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 6
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-16

Query Match      98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPCKGLEWVASITYDGSINY 60
QY 61 ADSVKGREITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPAPEL 238
QY 241 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTRYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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QY 61 ADSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120
Db 61 NPSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCPAPEL 238
QY 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 451

RESULT 8
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296.005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAIVSYGYSITSGYSNWIRQAPGKLEWVASITYDGSTNY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAIVSYGYSITSGYSNWIRQAPGKLEWVASITYDGSTNY 60
QY 61 ADSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120
Db 61 NPSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCPAPEL 238
QY 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 451

Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 451

RESULT 9
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296.005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-16

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAIVSYGYSITSGYSNWIRQAPGKLEWVASITYDGSTNY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAIVSYGYSITSGYSNWIRQAPGKLEWVASITYDGSTNY 60
QY 61 ADSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120
Db 61 NPSVKGRTISRDDSKNTFYLOMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCPAPEL 238
QY 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSPGK 451

Db 419 SRWQOQNVFSCSYMHHEALHNHYTKSLSPGK 451

RESULT 10

US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5994511

GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-18.

Query Match

Best Local Similarity 97.4%; Score 2369; DB 2; Length 451;

Mismatches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWVASITVDGSTNY 60

DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWVASIKYSGETKY 60

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120

DB 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120

QY 121 SASPKGKPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVL 180

DB 121 SASPT--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHCTCPCPAPEL 240

DB 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHCTCPCPAPEL 238

QY 241 LGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

DB 239 LGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 360

DB 299 QYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSEFFLYSKLTVDK 420

DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSEFFLYSKLTVDK 418

QY 421 SRWQOQNVFSCSYMHHEALHNHYTKSLSPGK 453

DB 419 SRWQOQNVFSCSYMHHEALHNHYTKSLSPGK 451

RESULT 11

US-09-109-207C-18

; Sequence 18, Application US/09109207C

; Patent No. 6172213

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept

; FILE REFERENCE: P1123R1

; CURRENT APPLICATION NUMBER: US/09/109,207C

; CURRENT FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/051,554

; PRIOR FILING DATE: 1997-07-03

; NUMBER OF SEQ ID NOS: 44

; SEQ ID NO 18

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; NAME/KEY: Artificial

; LOCATION: 1-451

; OTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-109-207C-18

Query Match

Best Local Similarity 97.4%; Score 2369; DB 3; Length 451;

Mismatches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWVASITVDGSTNY 60

DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKLEWVASIKYSGETKY 60

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120

DB 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 120

QY 121 SASPKGKPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVL 180

DB 121 SASPT--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHCTCPCPAPEL 240

DB 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHCTCPCPAPEL 238

QY 241 LGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

DB 239 LGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 360

DB 299 QYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQGPPEQVYITLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSEFFLYSKLTVDK 420

DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSEFFLYSKLTVDK 418

RESULT 12

US-09-282-505-2

; Sequence 2, Application US/09282505A

; Patent No. 6194551

; GENERAL INFORMATION:

; APPLICANT: Esophageal Idusogie et al.

; TITLE OF INVENTION: Polypeptide Variants

FILE REFERENCE: p1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INFORMATION: Sequence is completely synthesized
Patent No. 6194551
US-09-282-505-2

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.1e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWASITYDGSTNY 60
Db 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWASIKYGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTVS 120
QY 121 SASTKKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTTTPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTTTPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPCPAPEL 238
QY 241 LGGPSVFLPAPSKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Db 239 LGGPSVFLPAPSKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 418
QY 421 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-054-255-2
Sequence 2, Application US/09054255
Patent No. 6242195
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: polypeptide Variants
FILE REFERENCE: p1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INFORMATION: E27 anti-IgE antibody heavy chain
US-09-054-255-2

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.1e-179;

Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWASITYDGSTNY 60
Db 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWASIKYGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTVS 120
QY 121 SASTKKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTTTPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTTTPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTHTCPCPAPEL 238
QY 241 LGGPSVFLPAPSKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Db 239 LGGPSVFLPAPSKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSKLTVDK 418
QY 421 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 14
US-09-296-005-18
Sequence 18, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypepti
FILE REFERENCE: p1123C1f
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 18
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-18

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.1e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWASITYDGSTNY 60
Db 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWASIKYGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTVS 120
QY 121 SASTKKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTTTPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTTTPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPEL 240
|||||
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPEL 238
|||||
QY 241 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||||
Db 239 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
|||||
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 360
|||||
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 358
|||||
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
|||||
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
|||||
QY 421 SRWQOGNVFSCSYMHHEALHNHYTQKSLSLSPGK 453
|||||
Db 419 SRWQOGNVFSCSYMHHEALHNHYTQKSLSLSPGK 451
|||||

RESULT 15

US-09-282-846-2
; Sequence 2, Application: US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogle et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: FI266R2
; CURRENT APPLICATION NUMBER: US/09/282,846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-2

Query Match 97.4%; Score 2369; DB 4; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.1e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPKGLEWVASITYDGTNY 60
|||||
Db 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPKGLEWVASIKYGETKY 60
|||||
QY 61 ADSVKGRFTISRDDSKNTFYLOMNSLRAREDYAVYICARGSHYFGHHFAVWGQGLTVTVS 120
|||||
Db 61 NPSVKGRTISRDDSKNTFYLOMNSLRAREDYAVYICARGSHYFGHHFAVWGQGLTVTVS 120
|||||
QY 121 SASTKGKPSVFPPLAPSSKSTSGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
|||||
Db 121 SAST--KGPSVFPPLAPSSKSTSGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
|||||
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPEL 240
|||||
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPEL 238
|||||
QY 241 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||||
Db 239 LGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
|||||
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 360
|||||
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPS 358
|||||
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
|||||

| | | | |
|----|-----|---|-----|
| Qy | 61 | ADSVKGRFTISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFVAMVGQGLTVTYS | 120 |
| Db | | | |
| Qy | 61 | ADSVKGRFTISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFVAMVGQGLTVTYS | 120 |
| Db | | | |
| Qy | 121 | SASTKKGKGSVPFLAPSSKSTSGGTAALGCLIVKDYFPEPPTVTSWNSGALTSGVHTTTPAVL | 180 |
| Db | | | |
| Qy | 121 | SASTKKGKGSVPFLAPSSKSTSGGTAALGCLIVKDYFPEPPTVTSWNSGALTSGVHTTTPAVL | 180 |
| Db | | | |
| Qy | 181 | QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTVDKKVEPKSCDKTHTCPCPAPEL | 240 |
| Db | | | |
| Qy | 181 | QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTVDKKVEPKSCDKTHTCPCPAPEL | 240 |
| Db | | | |
| Qy | 241 | LGGPSVFLPPPKDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPRE | 300 |
| Db | | | |
| Qy | 241 | LGGPSVFLPPPKDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPRE | 300 |
| Db | | | |
| Qy | 301 | QYNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAIPAEIKTIISKAKGQPREPVYTLPPS | 360 |
| Db | | | |
| Qy | 301 | QYNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAIPAEIKTIISKAKGQPREPVYTLPPS | 360 |
| Db | | | |
| Qy | 361 | REEMTKNOVSLTCLVKGFYPSDIAVENESGQPENNYKTTTPVLDSDGSFFLYSKLTVDK | 420 |
| Db | | | |
| Qy | 361 | REEMTKNOVSLTCLVKGFYPSDIAVENESGQPENNYKTTTPVLDSDGSFFLYSKLTVDK | 420 |
| Db | | | |
| Qy | 421 | SRWQOQNFVSCSVMHAEALHNHYTQKSLSLSPGK | 453 |
| Db | | | |
| Qy | 421 | SRWQOQNFVSCSVMHAEALHNHYTQKSLSLSPGK | 453 |
| Db | | | |

RESULT 2
US-09-802-096-8
: Sequence 8, Application US/09802096
: Patent No. US20010038839A1
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
: FILE REFERENCE: P0718P2C3US
: CURRENT APPLICATION NUMBER: US/09/802,096
: CURRENT FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: US 08/405,617
: PRIOR FILING DATE: 1995-03-15
: PRIOR APPLICATION NUMBER: US 08/185,899
: PRIOR FILING DATE: 1994-01-26
: PRIOR APPLICATION NUMBER: PCT/US92/06860
: PRIOR FILING DATE: 1992-08-14
: PRIOR APPLICATION NUMBER: US 07/879,495
: PRIOR FILING DATE: 1992-05-07
: PRIOR APPLICATION NUMBER: US 07/744,768
: PRIOR FILING DATE: 1991-08-14
: NUMBER OF SEQ ID NOS: 64
: SEQ ID NO 8
: LENGTH: 453
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: humanized maeII, version 1 heavy chain
US-09-802-096-8

| | | | |
|---------------------------------------|-----|---|-----|
| Db | 121 | SASTKGKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTPAVL | 180 |
| QY | 181 | QSSGLYSLSVVTVPSSSLGTTQYICNVNHKESNTKVDKKVEPKSCDKTHTTCCPPAPEL | 240 |
| Db | 181 | QSSGLYSLSVVTVPSSSLGTTQYICNVNHKESNTKVDKKVEPKSCDKTHTTCCPPAPEL | 240 |
| QY | 241 | LGGPSVFLEPPKPKDLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE | 300 |
| Db | 241 | LGGPSVFLEPPKPKDLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE | 300 |
| QY | 301 | QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS | 360 |
| Db | 301 | QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS | 360 |
| QY | 361 | REEMTKNQVSLTCLVKGYGPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK | 420 |
| Db | 361 | REEMTKNQVSLTCLVKGYGPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK | 420 |
| QY | 421 | SRWQQGNVFCFSVMHEALHNHYTOKSLSLSPGK | 453 |
| Db | 421 | SRWQQGNVFCFSVMHEALHNHYTOKSLSLSPGK | 453 |
| RESULT 3 | | | |
| US-09-925-179-8 | | | |
| ; Sequence 8, Application US/09925179 | | | |
| ; Publication No. US20030044858A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Jardieu, Paula M. | | | |
| ; APPLICANT: Presta, Leonard G. | | | |

```

RESULT 3
US-09-925-179--8
; Sequence 8, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1CIUS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-925-179--8

```

| | Query Match | 100.0%; | Score 2432; | DB 11; | Length 453; |
|--------|---------------------------|--------------|-------------------|------------|-------------|
| | Best Local Similarity | 100.0%; | Pred. No. 1e-162; | | |
| | Matches 453; | Conservative | 0; | Mismatches | 0; |
| | | | | Indels | 0; |
| | | | | | |
| 1 QY | 1 EVQLVESGGGLVQPGGSLRLSCA | VSYITTS | GSYNNWIRQAPGKGL | EWASIT | YDGS |
| 1 Db | 1 EVQLVESGGGLVQPGGSLRLSCA | VSYITTS | GSYNNWIRQAPGKGL | EWASIT | YDGS |
| 61 QY | 61 ADSVKGRTTISRDDSKNTFY | LOMNSLR | AEADTAVYIC | ARGSHYFG | HHFAVWG |
| 61 Db | 61 ADSVKGRTTISRDDSKNTFY | LOMNSLR | AEADTAVYIC | ARGSHYFG | HHFAVWG |
| 121 QY | 121 SASITGKGPSVFPFLAPSSK | STSGGTA | ALGCLVKDY | FPPEPTV | SVSNWGALTS |
| 121 Db | 121 SASITGKGPSVFPFLAPSSK | STSGGTA | ALGCLVKDY | FPPEPTV | SVSNWGALTS |
| 181 QY | 181 QSSGLYSIVSSVVTVPSS | LGITQTY | ICNVNHKPS | NTKVDK | KVPEPKSCDK |
| | | | | | |

Db 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 240
QY 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTRPRE 300
Db 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTRPRE 300
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 361 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 453
Db 421 SRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 453

RESULT 4

US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7 5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVLVESGGGLVQPGLSLRSLSCAVSGYSITSGYSWNWIRQAPGKGLEWASITDGSNTY 60
Db 1 EVLVESGGGLVQPGLSLRSLSCAVSGYSITSGYSWNWIRQAPGKGLEWASITDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 238
QY 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTRPRE 300
Db 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTRPRE 300
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

QY 361 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 5

US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7 5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVLVESGGGLVQPGLSLRSLSCAVSGYSITSGYSWNWIRQAPGKGLEWASITDGSNTY 60
Db 1 EVLVESGGGLVQPGLSLRSLSCAVSGYSITSGYSWNWIRQAPGKGLEWASITDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKHTHTCCPPAPEL 238
QY 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTRPRE 300
Db 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTRPRE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 6

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US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of Tabl
US-09-925-179-65

Query Match          98.3%; Score 2391; DB 11; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGSGYSITSGYSWNIROAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAIVGSGYSITSGYSWNIROAPGKLEWVASITVDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFFLQNSLRAEDTAVYYCARGSHYFGHHFAVWGOGTLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFFLQNSLRAEDTAVYYCARGSHYFGHHFAVWGOGTLTVTS 120

QY 121 SASTKGKPSVFPPLAPSSKTSGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKTSGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178

QY 181 QSSGLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTCCPCPAPEL 240
DB 179 QSSGLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTCCPCPAPEL 238

QY 241 LGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
DB 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 7
US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of Tabl
US-09-925-179-66

Query Match          98.3%; Score 2391; DB 11; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGSGYSITSGYSWNIROAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAIVGSGYSITSGYSWNIROAPGKLEWVASITVDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFFLQNSLRAEDTAVYYCARGSHYFGHHFAVWGOGTLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFFLQNSLRAEDTAVYYCARGSHYFGHHFAVWGOGTLTVTS 120

QY 121 SASTKGKPSVFPPLAPSSKTSGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKTSGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178

QY 181 QSSGLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTCCPCPAPEL 240
DB 179 QSSGLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTCCPCPAPEL 238

QY 241 LGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 8
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of T
US-09-925-179-66

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; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
US-09-925-179-68

Query Match          97.8%; Score 2379; DB 11; Length 451;
Best Local Similarity 97.8%; Pred. No. 5.2e-159;
Matches 443; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSNY 60
QY 61 ADSVKGRTISRDDSKNTFYLOMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTVS 120
DB 61 NDSLKGRITISRDDSKNTFYLOMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPPCPAPEL 240
DB 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
DB 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLIHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLIHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQOGNFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQOGNFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01

; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
US-09-925-179-68

Query Match          97.8%; Score 2379; DB 11; Length 451;
Best Local Similarity 97.8%; Pred. No. 5.2e-159;
Matches 443; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSNY 60
QY 61 ADSVKGRTISRDDSKNTFYLOMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTVS 120
DB 61 NDSLKGRITISRDDSKNTFYLOMNSLRADTAAYYCARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPPCPAPEL 240
DB 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNPKVDKVPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLIHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLIHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQOGNFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQOGNFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-726-258-71
; Sequence 71, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-726-258-71

Query Match 91.1%; Score 2214.5; DB 11; Length 452;
Best Local Similarity 92.7%; Pred. No. 1.8e-147;
Matches 422; Conservative 8; Mismatches 20; Indels 5; Gaps 4;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITTSYSNWIRQAPGKLEWVAST-TYDGSIN 59
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHY-MHWVRQAPGKLEWVGIDPSNGETT 59
QY 60 YADSVKGRFTISRDDSKNTFYIOMNSLRAEDTAVYYCARGSH-YFGHHFAVWGQGLTV 118
Db 60 YNQKFKGRFTLSRDRSKNTAYLQMNLSRAEDTAVYYCARGDYRNGDWFDFVWGQGLTV 119
QY 119 VSSASTKGGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVGHVTPA 178
Db 120 VSSAST--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVGHVTPA 177
QY 179 VLQSSGLYSLSVWVPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPCPAP 238
Db 178 VLQSSGLYSLSVWVPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPCPAP 237
QY 239 ELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db 238 ELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 297
QY 299 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 358
Db 298 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 357
QY 359 PSREMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTV 418
Db 358 PSREMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTV 417
QY 419 DKSRWQOGNPFVSCVMHEALHNNHYTKQSLSPGK 453
Db 418 DKSRWQOGNPFVSCVMHEALHNNHYTKQSLSPGK 452

RESULT 11
US-10-020-786-11
Sequence 11, Application US/10020786
Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.

TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: anti-VEGF heavy chain
US-10-020-786-11

Query Match 90.9%; Score 2210; DB 15; Length 476;
Best Local Similarity 92.3%; Pred. No. 3.9e-147;
Matches 421; Conservative 6; Mismatches 23; Indels 6; Gaps 4;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITTSYSNWIRQAPGKLEWVAST-TYDGSIN 59
Db 24 EVQLVESGGGLVQPGGSLRLSCAASGYDFTH-YGNWVRQAPGKLEWVGWINTYGEPT 82
QY 60 YADSVKGRFTISRDDSKNTFYIOMNSLRAEDTAVYYCARGSHYFG--HWHFAVWGQGLTV 117
Db 83 YAADFKRFTFSLDTSKSTAYLQMNLSRAEDTAVYYCAKPYPYGTSHWYEDVWGQGLTV 142
QY 118 TVSSASTKGGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVGHVTP 177
Db 143 TVSSAST--KGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVGHVTP 200
QY 178 AVLQSSGLYSLSVWVPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPCPAP 237
Db 201 AVLQSSGLYSLSVWVPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPCPAP 260
QY 238 PELGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 297
Db 261 PELGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
QY 298 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 357
Db 321 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 380
QY 358 PSREMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLT 417
Db 381 PSREMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLT 440
QY 418 VDKSRWQOGNPFVSCVMHEALHNNHYTKQSLSPGK 453
Db 441 VDKSRWQOGNPFVSCVMHEALHNNHYTKQSLSPGK 476

RESULT 12
US-09-736-371B-21
Sequence 21, Application US/09736371B
Patent No. US20020131968A1
GENERAL INFORMATION:
APPLICANT: Waldmann, Herman
APPLICANT: Frewin, Mark
TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
FILE REFERENCE: Waldmann
CURRENT APPLICATION NUMBER: US/09/736,371B
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 9815909.8
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 21
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapiens

US-09-736-371B-21

Query Match 89.7%; Score 2182; DB 10; Length 449;
Best Local Similarity 91.9%; Pred. No. 3.3e-145;
Matches 417; Conservative 12; Mismatches 19; Indels 6; Gaps 4;

QY 1 EVOLVESGGGLVQPGGSLRLSCLAVSGYSITSGYSNWIRQAPGKLEWVASI--TYDGSN 59
DB 1 EVOLVESGGGLVQPGGSLRLSCLAVSGYSITSGYSNWIRQAPGKLEWVASI--TYDGSN 59
QY 60 YADSVKGRFTISRDDSKNTFYLMNSLRADETAVYICARGSHYFGHHFAV--WGQGTIV 119
DB 60 YRDSVKGRFTISRDDSKNTFYLMNSLRADETAVYICARGSHYFGHHFAV--WGQGTIV 117
QY 120 SSASTKKGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 179
DB 118 SSAST--KGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 175
QY 180 LQSSGLYSLSVSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239
DB 176 LQSSGLYSLSVSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
QY 240 LIGGSPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTPRE 299
DB 236 LIGGSPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTPRE 295
QY 300 EQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
DB 296 EQYASTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
QY 360 SREEMTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419
DB 356 SRDELTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
QY 420 KSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPGK 453
DB 416 KSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPGK 449

RESULT 13

US-10-253-366-2
; Sequence 2, Application US/10253366
; Publication No. US20030078388A1
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: FI241R1
; CURRENT APPLICATION NUMBER: US/10/253,366
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.

US-10-253-366-2

Query Match 89.6%; Score 2179.5; DB 15; Length 449;
Best Local Similarity 92.3%; Pred. No. 5e-145;
Matches 420; Conservative 9; Mismatches 17; Indels 9; Gaps 5;

QY 1 EVOLVESGGGLVQPGGSLRLSCLAVSGYSITSGYSNWIRQAPGKLEWVASI--TYDGSN 59
DB 1 EVOLVESGGGLVQPGGSLRLSCLAVSGYSITSGYSNWIRQAPGKLEWVASI--TYDGSN 59
QY 60 YADSVKGRFTISRDDSKNTFYLMNSLRADETAVYICARGSHYFGHHFAV--WGQGTIV 117
DB 60 YADSVKGRFTISRDDSKNTFYLMNSLRADETAVYICARGSHYFGHHFAV--WGQGTIV 116

QY 118 TVSSASTKKGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 297
DB 117 TVSSAST--KGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 294
QY 178 AVLOSSGLYSLSVSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPA 237
DB 175 AVLOSSGLYSLSVSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPA 234
QY 238 PELLGSPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 297
DB 235 PELLGSPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 294
QY 298 REEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 357
DB 295 REEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 354
QY 358 PPSREEMTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 417
DB 355 PPSREEMTKNQVSLTCLVKGYFSPDAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 414
QY 418 VDKSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPG 452
DB 415 VDKSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPG 449

RESULT 14

US-10-316-694-2
; Sequence 2, Application US/10316694
; Publication No. US20030118583A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, JEFFERSON C.
; APPLICANT: MCDONALD, PAUL J.
; APPLICANT: O'LEARY, RHONA M.
; TITLE OF INVENTION: STABILIZING POLYPEPTIDES WHICH HAVE BEEN EXPOSED TO UREA
; FILE REFERENCE: PI940R1
; CURRENT APPLICATION NUMBER: US/10/316,694
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/341,891
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.

US-10-316-694-2

Query Match 89.6%; Score 2179.5; DB 15; Length 449;
Best Local Similarity 92.3%; Pred. No. 5e-145;
Matches 420; Conservative 9; Mismatches 17; Indels 9; Gaps 5;

QY 1 EVOLVESGGGLVQPGGSLRLSCLAVSGYSITSGYSNWIRQAPGKLEWVASI--TYDGSN 59
DB 1 EVOLVESGGGLVQPGGSLRLSCLAVSGYSITSGYSNWIRQAPGKLEWVASI--TYDGSN 59
QY 60 YADSVKGRFTISRDDSKNTFYLMNSLRADETAVYICARGSHYFGHHFAV--WGQGTIV 117
DB 60 YADSVKGRFTISRDDSKNTFYLMNSLRADETAVYICARGSHYFGHHFAV--WGQGTIV 116
QY 118 TVSSASTKKGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 297
DB 117 TVSSAST--KGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 294
QY 178 AVLOSSGLYSLSVSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPA 237
DB 175 AVLOSSGLYSLSVSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPA 234
QY 238 PELLGSPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 297
DB 235 PELLGSPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKTP 294
QY 298 REEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 357

Job time : 50.608 secs

```

Db      295 REEQNSTYRVSVLTVLHODWLNKREYCKVSNKALPAIEKTIKAKGQPREPQVYTL 354
QY      358 PSREEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 417
Db      355 PSREEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 414
QY      418 VDKSRWQOGNVFSCSVMHAEALHNNHYTKOKSLSLSPG 452
Db      415 VDKSRWQOGNVFSCSVMHAEALHNNHYTKOKSLSLSPG 449

RESULT 15
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR APPLICATION DATE: 2002-05-17
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6
```

```

Query Match      89.5%; Score 2177.5; DB 15; Length 444;
Best Local Similarity 91.2%; Pred. No. 6.8e-145;
Matches 415; Conservative 16; Mismatches 11; Indels 13; Gaps 5;

QY      1 EVOLVESGGGLVQPGGSLRLSCAVSIGYSINWIRQAPGKGLEWVASITVDGS-TN 59
Db      1 EVOLVESGGGLVQPGGSLRLSCAASGFTFS-YDMSVWQAPGKGLEWVSTISSGGSYTY 59
QY      60 YADSVKGRFTISRDDSKNTFEYLQWNSLRAREDYAVYICAR-GSHYFGHWHEFVWVGQGLT 118
Db      60 YLDSIKGRFTISRDNKNSLYLQWNSLRAREDYAVYICARQGLDY-----WGRGTLVT 111
QY      119 VSSASTKGKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Db      112 VSSAST--KGPSVFPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 169
QY      179 VLOSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNWKVDKVEPKSCDKTHTCPCPAP 238
Db      170 VLOSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNWKVDKVEPKSCDKTHTCPCPAP 229
QY      239 ELGGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db      230 ELGGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 289
QY      299 EEQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTL 358
Db      290 EEQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTL 349
QY      359 PSREEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 418
Db      350 PSREEMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 409
QY      419 DKSRWQOGNVFSCSVMHAEALHNNHYTKOKSLSLSPG 453
Db      410 DKSRWQOGNVFSCSVMHAEALHNNHYTKOKSLSLSPG 444
```

Search completed: August 12, 2003, 16:43:50

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:26:07 ; Search time 20.2534 Seconds
(without alignments)
2150.973 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVOLVESGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 1750 | 72.0 | 330 | 1 GHU | Ig gamma-1 chain C |
| 2 | 1625.5 | 66.8 | 377 | 2 A23511 | Ig gamma-3 chain C |
| 3 | 1623.5 | 66.8 | 377 | 2 A60764 | Ig gamma-3 chain C |
| 4 | 1599 | 65.7 | 326 | 1 G2HU | Ig gamma-2 chain C |
| 5 | 1585.5 | 65.2 | 327 | 1 G4HU | Ig gamma-4 chain C |
| 6 | 1507.5 | 62.0 | 444 | 2 FC4436 | monoclonal antibody |
| 7 | 1477 | 60.7 | 374 | 2 S69339 | Ig heavy chain V r |
| 8 | 1467 | 60.3 | 470 | 2 S22080 | Ig heavy chain pre |
| 9 | 1444 | 59.4 | 472 | 2 S31459 | Ig gamma-1 chain - |
| 10 | 1403.5 | 57.7 | 469 | 2 S37483 | Ig gamma-2a chain |
| 11 | 1403 | 57.7 | 446 | 2 S40295 | Ig gamma-2a chain |
| 12 | 1359 | 55.9 | 474 | 1 G2MS11 | Ig gamma-2b chain |
| 13 | 1345.5 | 55.3 | 475 | 2 S01321 | Ig gamma-2b chain |
| 14 | 1263 | 51.9 | 328 | 2 I47159 | Ig gamma 2a chain |
| 15 | 1257 | 51.7 | 328 | 2 I47160 | Ig gamma 2a chain |
| 16 | 1254 | 51.6 | 255 | 4 S31866 | Ig gamma-1 chain C |
| 17 | 1248 | 51.3 | 234 | 2 PT0207 | Ig gamma chain C r |
| 18 | 1231.5 | 50.6 | 323 | 1 GHRB | Ig gamma chain C r |
| 19 | 1231 | 50.6 | 328 | 2 I47158 | Ig gamma 1 chain C |
| 20 | 1227 | 50.5 | 328 | 2 I47161 | Ig gamma 3 chain C |
| 21 | 1202.5 | 49.4 | 329 | 1 G2GP | Ig gamma-2 chain C |
| 22 | 1162.5 | 47.8 | 308 | 2 C30554 | Ig heavy chain C r |
| 23 | 1157 | 47.6 | 289 | 1 G3HWT | Ig gamma-3 chain C |
| 24 | 1150 | 47.3 | 326 | 2 PS0017 | Ig gamma-1 chain C |
| 25 | 1142 | 47.0 | 324 | 1 G1MS | Ig gamma-1 chain C |
| 26 | 1142 | 47.0 | 329 | 1 G3MSC | Ig gamma-3 chain C |
| 27 | 1139.5 | 46.9 | 333 | 2 PS0018 | Ig gamma-2b chain |
| 28 | 1137 | 46.8 | 393 | 1 G1MSM | Ig gamma-1 chain C |
| 29 | 1131 | 46.5 | 398 | 1 G3MSM | Ig gamma-3 chain C |

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence-revision 18-Aug-1982 #text-change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113:235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A:Note: This sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2

A:Note: This sequence has the Gln(non-I) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

Igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, Q', 36-96, K', 98-115, O', 117-197, D', 199-238, D', 240, L', 242-268, E', 27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, R', 98-197, D', 199-238, E', 240, M', 242-266, D', 273-330 <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:

A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/disulfide bonds: #status experimental
F:103/disulfide bonds: interchain (to light chain) #status experimental
F:109,112/disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 72.0%; Score 1750; DB 1; Length 330;
Best Local Similarity 98.8%; Pred. No. 8.4e-95;
Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 122 ASTKGGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 58
QY 182 SSGLYSLSSVTVFPSSSLGTQTYICNVNKPSTKVDKVPKSCDTHTCPCPAPELL 241
Db 59 SSGLYSLSSVTVFPSSSLGTQTYICNVNKPSTKVDKVPKSCDTHTCPCPAPELL 118
QY 242 GGPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNVDGVEVHNKTKPREQ 301
Db 119 GGPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNVDGVEVHNKTKPREQ 178
QY 302 YNSTYRVSVLVTLHODWLNKKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSR 361
Db 179 YNSTYRVSVLVTLHODWLNKKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSR 238
QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 421
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 298
QY 422 RWOQGNVFCSVWHEALHNHYTQKSLSLSPGK 453
Db 299 RWOQGNVFCSVWHEALHNHYTQKSLSLSPGK 330

RESULT 2

A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1625.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 1.7e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKGGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 58
QY 182 SSGLYSLSSVTVFPSSSLGTQTYICNVNKPSTKVDKVPKSCDTHTCPCPAPELL 221
Db 59 SSGLYSLSSVTVFPSSSLGTQTYICNVNKPSTKVDKVPKSCDTHTCPCPEPK 118
QY 222 -----EPKSKDTHTCPCPAPELLGGPSVFLFPKPK 254
Db 119 SCDTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPCEPK 178
QY 255 DTLMIKRTPEVTCVVDVSHEDPEVKFNVDGVEVHNKTKPREQYNSTYRVSVLV 314
Db 179 DTLMIKRTPEVTCVVDVSHEDPEVKFNVDGVEVHNKTKPREQYNSTYRVSVLV 238
QY 315 LHODWLNKKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSREMTKNQVSLTCL 374
Db 239 LHODWLNKKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSREMTKNQVSLTCL 298
QY 375 VKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSV 434
Db 299 VKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSV 358
QY 435 HEALHNHYTQKSLSLSPGK 453
Db 359 HEALHNHYTQKSLSLSPGK 377

RESULT 3

A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1623.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 2,2e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKRGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSTKVDKKV----- 221
Db 59 SSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSTKVDKKVRLKTPGDTHTTCPRCPK 118

QY 222 -----EPKSCDKHTCCPCPAPELLGGPSVFLFPPPK 254
Db 119 SCDTPPPCPCPEKSCDTPPPCPCPEKSCDTPPPCPCPAPELLGGPSVFLFPPPK 178

QY 255 DTLMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNNAKTKPREEQYNSTYRVVSVLT 314
Db 179 DTLMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNNAKTKPREEQYNSTYRVVSVLT 238

QY 315 LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSREEMTKNQVSLTCL 374
Db 239 LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSREEMTKNQVSLTCL 298

QY 375 VKGYFSPDIAVWESNGQPNENYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 434
Db 299 VKGYFSPDIAVWESNGQPNENYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 358

QY 435 HEALHNHYTQKSLSLSPGK 453
Db 359 HEALHNRYTQKSLSLSPGK 377

RESULT 4
G4HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and d
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85,132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132

A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa; disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69084124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.7%; Score 1599; DB 1; Length 326;
Best Local Similarity 91.3%; Pred. No. 4.9e-86;
Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;

QY 122 ASTKRGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCCPCPAPELL 241
Db 59 SSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSTKVDKTVKVERKCCVE--CPPCPAPP-V 114

QY 242 GGSVFLFPKPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNNAKTKPREQ 301
Db 115 AGPSVFLFPKPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNNAKTKPREQ 174

QY 302 YNSTYRVSVSLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSR 361
Db 175 FNSTYRVSVSLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSR 234

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPNENYKTPPPVLDSDGSFFLYSKLTVDKS 421
Db 235 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPNENYKTPPPVLDSDGSFFLYSKLTVDKS 294

QY 422 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 295 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
B:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30,81-326 <PIN>
C:Genetics:
A:Gene: GDB: IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger aggregates.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.2%; Score 1585.5; DB 1; Length 327;
Best Local Similarity 91.0%; Pred. No. 3e-85;
Matches 302; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 122 ASTKRGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 181
Db 1 AST -KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHCTCPAPPELL 241
Db 59 SSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHCTCPAPPELL 115

QY 242 GGPSVFLPFPKPKDPTLMISRTPEVTCVVDVSHEDPEVFNWYDGVNHNKTPKPREQ 301
Db 116 GGPSVFLPFPKPKDPTLMISRTPEVTCVVDVSHEDPEVFNWYDGVNHNKTPKPREQ 175

QY 302 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
Db 176 FNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 235

QY 362 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 421
Db 236 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 295

QY 422 RMOQGNVFCVSNVMEALHNHYTQKSLSLSPGK 453
Db 296 RMOQGNVFCVSNVMEALHNHYTQKSLSLSPGK 327

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Kashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase activity. It is directed against the active site of the enzyme.
C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IM4>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 62.0%; Score 1507.5; DB 2; Length 444;
Best Local Similarity 61.7%; Pred. No. 1.4e-80;
Matches 284; Conservative 67; Mismatches 86; Indels 23; Gaps 9;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIYDGS---S 57
Db 1 EVQAVETGGGLVPRGNSLKLSCLTSGTF--SNYRMHWRQPPGKRLIEWIAVITVKSNDY 59

QY 58 TNYADSVKGRFTISRDDSKNTFTYLOMNSLRRAEDTAVYCYCARGSHYFGHHFAV--RG 115
Db 60 AKYAESVGRGFTISRDDSKSSVYLOMNRLEEDTAYIYCCRTP-----WYAMDCWGQGT 114

QY 116 LVTVSSASTKRGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHT 175
Db 115 SVIVSSAKT--TPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPTVTVNNGSLSSGVHT 172

QY 176 FPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHCTCP 234
Db 173 FPAVLQSD-LYTLSSSVTVPPSSSTWPTSETVTCNVAHPASSTKVDKIVPRDCG---CKPC 227

QY 235 -CPAPPELLGGPSVFLPFPKPKDPTLMISRTPEVTCVVDVSHEDPEVFNWYDGVNHN 293
Db 228 ICTVPEV---SSVFIIPPFPKPKDPTLTLPKVTCTVVDVSHEDPEVFNWYDGVNHN 284

QY 294 KYKPREQVNSYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREP 353
Db 285 QTQPREQVNSYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREP 344

QY 354 VTLTPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 413
Db 345 VTIPTPPKQMAKDKVSLTCTMTDTPEDITVEMQWNGQPAENYKNTQIPMDTDSGFYV 404

QY 414 SKLTVDKSRWQGNVFCVSNVMEALHNHYTQKSLSLSPGK 453
Db 405 SKLVNQSKEAGNFTCSVLHDEGLHNHNHTEKSLSPGK 444

RESULT 7
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 60.7%; Score 1477; DB 2; Length 374;
Best Local Similarity 63.5%; Pred. No. 7.1e-79;
Matches 289; Conservative 20; Mismatches 44; Indels 102; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSIT--SGYSWNIROAPGKLEWVASIYDGS 59
Db 20 QITLKESGFTLVKPNQTLTICTSGFSLSGVGVGVIROPPGQALEWIALIFWDDDKR 79

[illegible]

RESULT 8
S22080
Ig heavy chain precursor (B/MT 4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.

submitted to EMBL Data Library, November 1991

A:Reference number: S22080

A:Accession: S22080

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-470 <S>

A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989

A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma

A:Reference number: S06610; MUID:90097956; PMID:2513487

A:Accession: S06610

A:Molecule type: DNA

A:Residues: 142-470 <SYM>

A:Cross-references: EMBL:X16701

A>Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: Ig CH gamma-1

A:Introns: 98/1; 111/1; 221/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>

F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 60.3%; Score 1467; DB 2; Length 470;
Best Local Similarity 62.6%; Pred. No. 3.5e-78;
Matches 286; Conservative 58; Mismatches 103; Indels 10; Gaps

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Qy 119 VSSASTKGKGPSVFPEPLAPSSKSTSGGTAALGCLGVKDYFPEPVTVMNSNGALTSGVHTFPA 178
Db 139 VSSAST--TAPKYVPLSSCCGDKSSSTVTTLGCLVSSYMPBEVPTVMNSGALKSGVHTFPA 196
Qy 179 VLOSSGLYSLSSVVTVPSSSLGTQTYTCNVNHHKPSNTKVDKKVEPKSCDKTHTCPCPCAP 238
Db 197 VLOSSGLYSLSSMWTVPGSTSG-QTFCTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPP 253
Qy 239 ELGGPSVFLFPKPKDFTLMSRTPETCVVVOVSVEDPEVKFNMYVDGVVEVHNNAKTKPR 298
Db 254 ELPGGPSVFIFFPKPKDFTLISGTPEYTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPR 313
Qy 299 EEOVNSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPPREPQVYVTL 358
Db 314 EEOFNSTYRVVVSALRIQHODWTGCKEKKVHNEGLPAPIVTRISRTKGPAREQVIVLA 373
Qy 359 PSREEMTKNOVSLTCLVKGYPSDIAVEVNSNGP--ENNYKTTPTPVLDSGSGFFLYSKL 416
Db 374 PPOEELSKSTVSLTCMYTSEFYDPIAYEVRNGQPESEDKYGTGTPPQLDADSSYFLYSKL 433
Qy 417 TVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 434 RVDNSHQEGDYYTCVVVHEALHNHYTQKSSTKSAGK 470

RESULT 9
S31459
Iq gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
C;277-346/Domain: immunoglobulin homology <IMM>

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| | | | | |
|-----------------------|-------|---|------|----------------|
| Query Match | 59.4% | Score 1444 | DB 2 | Length 472 |
| Best Local Similarity | 59.9% | Pred. No. 7.6e-77 | | |
| Matches | 275 | Conservative | 64 | Mismatches 110 |
| | | | | Indels 10 |
| | | | | Gaps 5 |
| Qy | 1 | EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASITYDGSITNY | 60 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : | | |
| Db | 18 | QVRLQESGPSLATLQLTSLVCTITSGFSL-NNYGVDWVRQAPGKALEWLGSGGYDEIDY | 76 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : | | |
| Qy | 61 | ADSVKGRFTISRDSKNTFYIOMNSLRAREDYAVYYCAR- ---GSHYGHWHFAVWGQGLT | 116 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Db | 77 | NPVLKSLRSITKDTSKSQVSLTLSTVTATEDYAVYYCARVDYDSSHAFAYASYDFWGPGLL | 136 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Qy | 117 | VTWSSASTKGGPSVFFPLAPSSKTSGGTAALGCLVKDYDPEPTVYVSNWSGALTSGVHTF | 176 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Db | 137 | ISVLSAST--TPPKVYPLTSCGGITSSIVTLGCLVSSYMPETVYVTSNSGALTSGVHTF | 194 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Qy | 177 | PAVLQSGSLYSLSSVWVPSSLSGTQYICNVNHPKNTKYDKKVEPKSCDKTHTCPCP | 236 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Db | 195 | PAIQLQSGSLYSLSSVWVPASPASGAQTFICNVAHPASSTKYDKKVEKPPDPCPKHC-RCP | 253 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Qy | 237 | APELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNFNVDGVEVHNAKTK | 296 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Db | 254 | PPELGGSPSVFIFFPKPKDTLTISGTPEVTCVVDVGQDDPEQVQFMFVDNVEYRTARK | 313 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Qy | 297 | PREEOYNSTRVRSVSLTVLHODWLNGREYKCKVSNKALPAPIETKTSKAKGPPEQVYT | 356 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Db | 314 | PRESQFINSTRFKVRSALPIQHODWTGGKEFKCKVINEALPAPIVITISRTKGQAREQVYV | 373 | |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | | |
| Qy | 357 | LPPSREEMTKNOVSLTCLVKGFPSPDIADAVENSGQP--ENNYKTTTPVLDSGSGFFLYS | 414 | |

Db 374 LAPPOEELSKSTLSVCLVTGYDPDYIAVWQKNGQPESEDKYGTTSIQSLDADSGSYFLYS 433
QY 415 KLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453
Db 434 RLVDKNSQGGDYACVVMHEALHNHYTKSLSPGK 472

RESULT 10
S37483
Ig gamma-2a chain - mouse
A:Accession: S37483
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993

A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.7%; Score 1403.5; DB 2; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.7e-74;
Matches 270; Conservative 68; Mismatches 102; Indels 23; Gaps 8;

QY 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASTIYDGSNT 59
Db 20 QIQLOQSGPELVKPGASVKISCKASGYTFD-YINWVKQPGQGLKGIWYIPASGNTK 78
QY 60 YADSVKGRFTISRDDSKNTFYLQMNSLRADETAVYFCARG-----HYFGHWFAVWG 112
Db 79 YNEFKGKATLVDTSSSTAYMQLSLTSEDVAVFCARGATATLDY-----WG 130
QY 113 QGTLTVSSASPKGSPVFLPAPSSKSTSGTAALGCLVKDYFPEPTVSWNSGALTSG 172
Db 131 QGTLTVSSAKT--TAPSVPLAPVCGDTTGSSTGLVGLVGFPEPTVLTWNSGSLSSG 188
QY 173 VHTFPAVLQSSGLYSLSSVWVPSSSLGTQTYICNVNHPKNTKVKVEPKSCDKTHCT 232
Db 189 VHTFPAVLQSD-LYTLSSSVTVSTWPSQSIICNVNHPKNTKVKVEPKSCDKTHCT 246
QY 233 PP--CPAPELLGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVDGVEV 290
Db 247 PPCKPAPNLLGGPSVFLFPKPKIDVLMISLPIVTCVVDVSEDDPDVQISFVNVEV 306
QY 291 HNAKTKPREOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPR 350
Db 307 HTAQOTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIETISKPKGSVR 366
QY 351 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 410
Db 367 APQVYVLPPEEEMTKQVLTLCMTVDPEDIYVEWNNKTELNYKNTPEVLDSDGSY 426
QY 411 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453
Db 427 FMYSKLVRKKNWVNSYSCSVVHVEGLHNHHTTKFSRTPGK 469

RESULT 11
S40295
Ig gamma-2a chain (Mab735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B.
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295

A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; proglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CH1>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 57.7%; Score 1403; DB 2; Length 446;
Best Local Similarity 59.4%; Pred. No. 1.7e-74;
Matches 271; Conservative 67; Mismatches 104; Indels 14; Gaps 8;

QY 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASTIYDGS--T 58
Db 1 QIQLOQSGPELVKPGASVKISCKASGYTFD-YIHWVKQPGEGLEWIGWI-YPGSGNT 58
QY 59 NYADSVKGRFTISRDDSKNTFYLQMNSLRADETAVYFCARGSHYFGHWFAVWGGTSLVT 118
Db 59 KYNEFKGKATLVDTSSSTAYMQLSLTSEDVAVFCARG-----GXFAMDYWGCGTSVT 114
QY 119 VSSASTKKGSPVFLPAPSSKSTSGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Db 115 VSSAKT--TAPSVPLAPVCGDTTGSSTGLVGLVGFPEPTVLTWNSGSLSSGVHTFPA 172
QY 179 VQSSGLYSLSSVWVPSSSLGTQTYICNVNHPKNTKVKVEPKSCDKTHCTCPP--CP 236
Db 173 VQSSD-LYTLSSSVTVSTWPSQSIICNVNHPKNTKVKVEPKSCDKTHCTCPP--CP 236
QY 237 APPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVDGVEVHNAKTK 296
Db 231 APNLLGGPSVFLFPKPKIDVLMISLPIVTCVVDVSEDDPDVQISFVNVEVLTATQ 290
QY 297 PREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREQVYT 356
Db 291 THREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIETISKPKGSVRAPQVYV 350
QY 357 LPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKL 416
Db 351 LPPPEEMTKNQVLTLCMTVDPEDIYVEWNNKTELNYKNTPEVLDSDGSYFMYSKL 410
QY 417 TVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 452
Db 411 RVEKKNWVNSYSCSVVHVEGLHNHHTTKFSRTPG 446

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FTS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from a mouse
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
 A:Cross-references: GB:J00461
 A:Note: The sequence was determined from the germline gene
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain
 A:Reference number: A26235; MUID:80081501; PMID:117548
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
 A:Note: Lys-474 is probably removed posttranslationally
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin
 A:Reference number: A26232; MUID:80081502; PMID:117549
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
 R:Ollo, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b
 A:Reference number: A26233; MUID:82113203; PMID:6803173
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
 J. Biol. Chem. 269, 12345-12350, 1994
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359; PMID:7512967
 A:Accession: A53598
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 C:Comment: The a allele sequence is shown.
 C:Genetics:
 A:Introns: 138/1; 236/1; 258/1; 368/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
 F:137-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>
 F:367-454/Domain: immunoglobulin homology <IM3>
 F:152/disulfide bonds: interchain (to light chain) #status predicted
 F:164-220,288-348,394-452/disulfide bonds: #status predicted
 F:247,250,253,256/disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 55.9%; Score 1359; DB 1; Length 474;
 Best Local Similarity 56.7%; Pred. No. 6.6e-72;
 Matches 262; Conservative 71; Mismatches 113; Indels 16; Gaps 8;
 Qy 1 EVLVESGGGLVPGGSLRSCAVSGYSITSGYSWNNIRQAPGKLEWVASI--TYDGS 58
 Db 20 EVLQSGPELVNPGASVKMSCKASGYTFIT-VYMHVVKQPGGLEWICYINPNKDG-T 77
 Qy 59 NYADSVKGRFTISRDDSKNTFYLQMSLRADETAVYVCARGSHYFGHHFAVWGQGLTV 118
 Db 78 KFNEKFKGKATLTVDKSSNTAYMELSLTSDSAVYCARDYD--DW-FAYWGQGLTV 134
 Qy 119 VSSASTKKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSCVHTF 178
 Db 119 VSSASTKKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSCVHTF 178

135 VSAAKT--TPPSVYPLAPGCGDTTGSSTVSGCLVKGYFPESTVTWNSGLSSSVHTLSQ 192
 Qy 179 VLOSSGLYSSVVTPSSSLGTQTYTCNVNHRPSNTKVDKVPKPCDCKT-HTCPCP--- 234
 Db 193 ALLOSGLYTWSSSVTPSSSTWPSQTVCSTVAHPASSSTVDKLEPSPGISTINCPCKE 252
 Qy 235 ---CPAPPELLGGPSVFLFPPPKDMLSRPTPEVTVVVDVSHEDPEVKFNWYVDGEV 291
 Db 253 CHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPTKVTCTVVDVSEDDPDVQISFWNNVE 312
 Qy 292 NAKTKPREEOYNSTIRYVSVLTVLHODWLNCKEYCKVSNKALPAPIETKISKAKGP 351
 Db 313 TAQTQTHREDYNSTIRVVSALPIQHQDMSCKEFCCKVNNKDLPSPIERTISKIGLV 372
 Qy 352 PQVYTLPPSREEMTKNQVSLTCLVKGYFSPDAVWEESNGQPENNYKTPPVLDSDGSG 411
 Db 373 PQVYILPPAPAEOLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYKDTAPVLDSD 432
 Qy 412 LYSKLTVDKSRWQOGNVSFSCVMHEALHNHYTQKSLSLSPGK 453
 Db 433 IYSLNKNKTSKWEKTSDFSCNVRHEGLKNVYLKKTISRSPGK 474
 RESULT 13
 S01321
 Ig gamma-2b chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C:Accession: S01321
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 Eur. J. Biochem. 176, 287-295, 1988
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
 A:Reference number: S01320; MUID:88329081; PMID:3138116
 A:Accession: S01321
 A:Molecule type: mRNA
 A:Residues: 1-475
 A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
 A:Note: This sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMM>
 Query Match 55.3%; Score 1345.5; DB 2; Length 475;
 Best Local Similarity 56.7%; Pred. No. 4e-71;
 Matches 262; Conservative 72; Mismatches 113; Indels 15; Gaps 8;
 Qy 1 EVLVESGGGLVPGGSLRSCAVSGYSITSGYSWNNIRQAPGKLEWVASIYDGS 59
 Db 20 QVQLQSGAEELARPASVKLSCKASGYTLTS-YGISWVKQRTGGLEWIGEI-YPGSG 77
 Qy 60 -YADSVKGRFTISRDDSKNTFYLQMSLRADETAVYVCARGSHYFGHHFAVWGQGLTV 118
 Db 78 YFNEKFKGKATLTVDKSSNTAYLHLSLTSDSAVYFCA-GPROVGLLPFGYWGQGLTV 136
 Qy 119 VSSASTKKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSCVHTF 178
 Db 137 ASAAKT--TPPSVYPLAPGCGDTTGSSTVSGCLVKGYFPESTVTWNSGLSSSVHTF 194
 Qy 179 VLOSSGLYSSVVTPSSSLGTQTYTCNVNHRPSNTKVDKVPKPCDCKT-HTCPCP--- 234
 Db 195 LLQ-SGLYTWSSSVTPSSSTWPSQTVCSTVAHPASSSTVDKLEPSPGISTINCPCKE 253
 Qy 235 ---CPAPPELLGGPSVFLFPPPKDMLSRPTPEVTVVVDVSHEDPEVKFNWYVDGEV 291
 Db 254 CHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPTKVTCTVVDVSEDDPDVQISFWNNVE 313
 Qy 292 NAKTKPREEOYNSTIRYVSVLTVLHODWLNCKEYCKVSNKALPAPIETKISKAKGP 351
 Db 314 TAQTQTHREDYNSTIRVVSALPIQHQDMSCKEFCCKVNNKDLPSPIERTISKIGLV 373
 Qy 352 PQVYTLPPSREEMTKNQVSLTCLVKGYFSPDAVWEESNGQPENNYKTPPVLDSDGSG 411

Db 374 PQVYILSPPEQLSRKDVSLTCLAVGFSPELSDVWTSNGHTEENYKDTAPVLDSDGSYF 433
QY 412 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 453
Db 434 IYSKLNMTSKWEKTDSCNVRHGLKNYLLKTIISRSPGK 475

RESULT 14

I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 1263; DB 2; Length 328;
Best Local Similarity 70.3%; Pred. No. 1.7e-66;
Matches 230; Conservative 43; Mismatches 48; Indels 6; Gaps 2;

QY 129 PSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PSVYPLAPCSRDTSGPNVALGLASSYFPEPTVTWNSGALSSGVHTFPAVLQPSGLYSL 65
QY 189 SSVVTVPSSSLGTQTYICNVNHPSTNTKVDKVEPKSCDKHTCTPCPCPAPELLGGPSVFL 248
Db 66 SSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGTCTKPCPCPACESP---GPSVFI 121
QY 249 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 308
Db 122 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 181
QY 309 VSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRREEMTKNQ 368
Db 182 VSVLPIDHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRREEMTKNQ 241
QY 369 VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG 426
Db 242 VSITCLVIGFYPDPIDVEQNRNGQPEPEGNRYRTTPQQDVGDTYFLYKSFVSKASWQGG 301
QY 427 NVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 302 GIFQCAVMHEALHNHYTQKSISKTPGK 328

RESULT 15

I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C:Genetics:

A:Gene: IgG2b

C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 51.7%; Score 1257; DB 2; Length 328;
Best Local Similarity 70.0%; Pred. No. 3.7e-66;
Matches 229; Conservative 42; Mismatches 50; Indels 6; Gaps 2;

QY 129 PSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PLVYPLAPCGRDTSGPNVALGLASSYFPEPTVTWNSGALTSGVHTFPAVLQPSGLYSL 65
QY 189 SSVVTVPSSSLGTQTYICNVNHPSTNTKVDKVEPKSCDKHTCTPCPCPAPELLGGPSVFL 248
Db 66 SSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGTCTKPCPCPACESP---GPSVFI 121
QY 249 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 308
Db 122 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 181
QY 309 VSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRREEMTKNQ 368
Db 182 VSVLPIDHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRREEMTKNQ 241
QY 369 VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG 426
Db 242 VSITCLVIGFYPDPIDVEQNRNGQPEPEGNRYRTTPQQDVGDTYFLYKSFVSKASWQGG 301
QY 427 NVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 302 GIFQCAVMHEALHNHYTQKSISKTPGK 328

Search completed: August 12, 2003, 16:32:18
Job time : 21.2534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:22:22 ; Search time 12.152 seconds
(without alignments)
1753.051 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVQLVSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPCK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Query % | Length | ID | Description |
|------------|--------|-------|---------|--------|------------|--------------------|
| 1 | 1750 | 72.0 | 330 | 1 | GCL_HUMAN | P01857 homo sapien |
| 2 | 1599 | 65.7 | 326 | 1 | GC2_HUMAN | P01859 homo sapien |
| 3 | 1585.5 | 65.2 | 327 | 1 | GC4_HUMAN | P01861 homo sapien |
| 4 | 1231.5 | 50.6 | 323 | 1 | GC_RABIT | P01870 oryctolagus |
| 5 | 1202.5 | 49.4 | 329 | 1 | GC2_CAVPO | P01862 cavia porce |
| 6 | 1162 | 47.8 | 290 | 1 | GC3_HUMAN | P01860 homo sapien |
| 7 | 1150 | 47.3 | 326 | 1 | GCL_RAT | P20759 rattus norv |
| 8 | 1142 | 47.0 | 324 | 1 | GCL_MOUSE | P01868 mus musculu |
| 9 | 1142 | 47.0 | 329 | 1 | GC3_MOUSE | P22436 mus musculu |
| 10 | 1139.5 | 46.9 | 333 | 1 | GCB_RAT | P20761 rattus norv |
| 11 | 1137 | 46.8 | 393 | 1 | GCL_MOUSE | P01869 mus musculu |
| 12 | 1131 | 46.5 | 398 | 1 | GC3_MOUSE | P03987 mus musculu |
| 13 | 1126 | 46.3 | 330 | 1 | GCAA_MOUSE | P01863 mus musculu |
| 14 | 1123.5 | 46.2 | 335 | 1 | GCAE_MOUSE | P01864 mus musculu |
| 15 | 1121 | 46.1 | 399 | 1 | GCAM_MOUSE | P01865 mus musculu |
| 16 | 1117.5 | 45.9 | 329 | 1 | GCC_RAT | P20762 rattus norv |
| 17 | 1110 | 45.6 | 322 | 1 | GCA_RAT | P20760 rattus norv |
| 18 | 1082 | 44.5 | 336 | 1 | GCB_MOUSE | P01866 mus musculu |
| 19 | 1077 | 44.3 | 405 | 1 | GCB_MOUSE | P01867 mus musculu |
| 20 | 482.5 | 19.8 | 429 | 1 | EPC_RAT | P01855 rattus norv |
| 21 | 478 | 19.7 | 428 | 1 | EPC_HUMAN | P01854 homo sapien |
| 22 | 468 | 19.2 | 421 | 1 | EPC_MOUSE | P06336 mus musculu |
| 23 | 441 | 18.1 | 454 | 1 | MUC_HUMAN | P01871 homo sapien |
| 24 | 439.5 | 18.1 | 122 | 1 | HV3C_HUMAN | P01768 homo sapien |
| 25 | 437.5 | 18.0 | 458 | 1 | MUC_RABIT | P03988 oryctolagus |
| 26 | 431.5 | 17.7 | 455 | 1 | MUC_MOUSE | P01872 mus musculu |
| 27 | 427.5 | 17.6 | 479 | 1 | MUCM_RABIT | P04221 oryctolagus |
| 28 | 421.5 | 17.3 | 476 | 1 | MUCM_MOUSE | P01873 mus musculu |
| 29 | 421 | 17.3 | 119 | 1 | HV3I_HUMAN | P01770 homo sapien |
| 30 | 420 | 17.3 | 123 | 1 | HV24_MOUSE | P01793 mus musculu |
| 31 | 419 | 17.2 | 120 | 1 | HV3E_HUMAN | P01766 homo sapien |
| 32 | 418 | 17.2 | 457 | 1 | MUC_SUNMU | P20768 suncus muri |
| 33 | 415.5 | 17.1 | 114 | 1 | HV3B_HUMAN | P01763 homo sapien |

ALIGNMENTS

RESULT 1

| ID | GCL_HUMAN | STANDARD; | PRT; | 330 AA. |
|----|--|-----------|------|---------|
| AC | P01857; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ig gamma-1 chain C region. | | | |
| GN | IGHG1. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=82274238; PubMed=6287432; | | | |
| RA | Ellison J.W., Berson B.J., Hood L.E.; | | | |
| RT | "The nucleotide sequence of a human immunoglobulin C gamma1 gene."; | | | |
| RL | Nucleic Acids Res. 10:4071-4079(1982). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | | |
| RX | MEDLINE=71064024; PubMed=5489771; | | | |
| RA | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., | | | |
| RA | Waxdal M.J., Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; | | | |
| RN | Biochemistry 9:3161-3170(1970). | | | |
| RN | [3] | | | |
| RP | SEQUENCE OF 136-329 (EU). | | | |
| RX | MEDLINE=71064025; PubMed=5530842; | | | |
| RA | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., | | | |
| RA | Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; | | | |
| RL | Biochemistry 9:3171-3181(1970). | | | |
| RN | [4] | | | |
| RP | SEQUENCE (MYELOMA PROTEIN NIE). | | | |
| RX | MEDLINE=77070269; PubMed=826475; | | | |
| RA | Ponstingl H., Hilschmann N.; | | | |
| RT | "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; | | | |
| RL | Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). | | | |
| RN | [5] | | | |
| RP | SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. | | | |
| RX | MEDLINE=83289131; PubMed=6884994; | | | |
| RA | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; | | | |
| RT | "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; | | | |
| RL | Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). | | | |
| RN | [6] | | | |
| RP | DISULFIDE BONDS. | | | |
| RX | MEDLINE=71064027; PubMed=4923144; | | | |
| RA | Gall W.E., Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. X. | | | |

P01874 canis famil
P06337 mesocricetu
P01771 homo sapien
P01767 homo sapien
P01765 homo sapien
P19181 carassius a
P01769 homo sapien
P01791 mus musculu
P01781 homo sapien
P01782 homo sapien
P01799 mus musculu
P04220 homo sapien

MUC_CANFA
MUC_MESAU
HV3I_HUMAN
HV3E_HUMAN
HV3D_HUMAN
HV05_CARAU
HV3H_HUMAN
HV22_MOUSE
HV3T_HUMAN
HV3U_HUMAN
HV30_MOUSE
MUCB_HUMAN

34 414 17.0 450 1
35 413.5 17.0 454 1
36 413 17.0 121 1
37 412 16.9 115 1
38 410 16.9 115 1
39 406.5 16.7 116 1
40 405.5 16.7 122 1
41 405 16.7 123 1
42 404.5 16.6 116 1
43 403.5 16.6 120 1
44 403 16.6 113 1
45 403 16.6 391 1

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 CC EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR PDB; 1AJ7; 12-NOV-97.
 DR PDB; 1D5B; 09-FEB-00.
 DR PDB; 1D51; 09-FEB-00.
 DR PDB; 1D6V; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1E4K; 06-JUN-01.
 DR PDB; 1FCC; 20-JUL-95.
 DR PDB; 1HZH; 12-JUN-02.
 DR PDB; 1I72; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100;
 DR GO; GO:0005624; C-membrane fraction; NAS.
 DR GO; GO:0003823; F-antigen binding activity; TAS.
 DR GO; GO:0006953; P-immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG-LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 122 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 147
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 166
 FT TURN 168 171
 FT STRAND 176 179
 FT TURN 180 181
 FT STRAND 182 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 242
 FT STRAND 245 256
 FT STRAND 260 285
 FT STRAND 270 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT TURN 297 301
 FT STRAND 302 303
 FT STRAND 305 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 325
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 72.0%; Score 1750; DB 1; Length 330;
 Best Local Similarity 98.8%; Pred. No. 5,1e-113;
 Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
 QY 122 ASTKGKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
 Db 1 AST--KGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58
 QY 182 SSGLYSLSSVTVPSSSLGCTQTYICNVNHPKSNTPKVKKVEPKSCDKHTCPCPAPELL 241
 Db 59 SSGLYSLSSVTVPSSSLGCTQTYICNVNHPKSNTPKVKKVEPKSCDKHTCPCPAPELL 118
 QY 242 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 301
 Db 119 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 178
 QY 302 YNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
 Db 179 YNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 238
 QY 362 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSGSEFLYSLKLTVDKS 421
 Db 239 DELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSGSEFLYSLKLTVDKS 298

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QY 422 RWOQGNVSCVMHEALHNNHYTKSLSPGK 453
Db 299 RWOQGNVSCVMHEALHNNHYTKSLSPGK 330

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
[2]
"Linkage and sequence homology of two human immunoglobulin gamma
heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
[3]
SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RC MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679(1982).
[4]
SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RC MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407(1982).
[5]
SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
[6]
SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
[7]
SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
[8]
REVIEWS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
[9]
SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";

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RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC -----
CC EMBL; J00230; AAB59393.1;
DR PIR; A93906; G2HU.
DR HSSP; P01857; IFC1.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110;
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
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FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 8310878C6878CF9C CRC64;
SQ
Query Match 65.7%; Score 1599; DB 1; Length 326;
Best Local Similarity 91.3%; Pred. No. 1.1e-102;
Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;
QY 122 ASTKGKSPVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGSPVPLAPCSNSTESAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 58
QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVPEPKSCDKTHTCPPCPAPPELL 241
Db 59 SSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVPEPKSCDKTHTCPPCPAPPELL 114
QY 242 GGPSVFLFPKPKDPTLMISRTPEVTVCVVVDVSHEDPEVKFNWYVDGEVHNNAKTKPREEQ 301
Db 115 AGPSVFLFPKPKDPTLMISRTPEVTVCVVVDVSHEDPEVKFNWYVDGEVHNNAKTKPREEQ 174

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QY 302 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR 361
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Db 175 FNSTFRVSVLTVVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR 234

QY 362 EEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 421
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 EEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 294

QY 422 RWOOGNPFVSCVMHEALHNYTKQSLSPGK 453
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 RWOOGNPFVSCVMHEALHNYTKQSLSPGK 326

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
RN [3]
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
RN [4]
RP EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; IADQ; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130;
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGH1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 65.2%; Score 1585.5; DB 1; Length 327;
Best Local Similarity 91.0%; Pred. No. 9.5e-102;
Matches 302; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 122 ASYKKGKPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ASYKKGKPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHCTCPCPAPELL 241
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHCTCPCPAPELL 115

QY 242 GGPSEVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 GGPSEVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 175

QY 302 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR 361
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR 235

QY 362 EEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 421
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 236 EEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 295

QY 422 RWOOGNPFVSCVMHEALHNYTKQSLSPGK 453
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 296 RWOOGNPFVSCVMHEALHNYTKQSLSPGK 327

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RESULT 4

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GC_RABIT
ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";

```


Biochem. J. 116:249-259(1970)).

[5] SEQUENCE OF 129-131 AND 155-322.

RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;

RL (In) Killander J. (eds.);

RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,

RL Stockholm (1967).

CC MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,

CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15

CC MARKERS AND REF.5 THE E15 MARKER.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

CC -----

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CC -----

DR EMBL; M16426; AAA31289.1; -.

DR PIR; A91749; GHRB.

DR HSSP; P01857; 1FCL.

DR InterPro; IPR007110; Ig-Like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00407; Igcl; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Repeat.

KW NON_TER 1 1

FT DOMAIN 1 96 IG-LIKE 1.

FT DOMAIN 6 96 IG-LIKE 2.

FT DOMAIN 114 213 IG-LIKE 3.

FT DOMAIN 222 318 T -> M (IN D11 MARKER).

FT VARIANT 104 104 T -> A (IN E15 MARKER).

FT VARIANT 185 185 N -> E (IN REF. 2).

FT CONFLICT 48 48 V -> VPV (IN REF. 2).

FT CONFLICT 71 71 Q -> E (IN REF. 3 AND 4).

FT CONFLICT 144 144 N -> D (IN REF. 5).

FT CONFLICT 173 173 Q -> E (IN REF. 3 AND 5).

FT CONFLICT 187 187 N -> D (IN REF. 5).

FT CONFLICT 201 201 N -> E (IN REF. 5).

FT CONFLICT 218 218 E -> Q (IN REF. 5).

FT CONFLICT 233 233 N -> D (IN REF. 5).

FT CONFLICT 246 246 E -> G (IN REF. 5).

FT CONFLICT 256 256 N -> D (IN REF. 5).

FT CONFLICT 260 260 Y -> W (IN REF. 5).

FT CONFLICT 266 266 Y -> S (IN REF. 5).

FT CONFLICT 280 280 N -> S (IN REF. 5).

FT CONFLICT 284 284

SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 50.6%; Score 1231.5; DB 1; Length 323;

Best Local Similarity 70.0%; Pred. No. 1.7e-77;

Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 127 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVNSNGALTSVHTFPAVLQSSGLY 186

DB 4 KAPSVFPLAPCGDTPSSTVTLGCLVKGLYPEPTVNSNGALTSVHTFPAVLQSSGLY 63

QY 187 SLSSVVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSKDTHCTCPQAPPELLGGPSV 246

DB 64 SLSSVVVTSSTSS--QPVTCTNVAHPATNTKVDKTVAPSTCSK---PTCPPPELLGGPSV 116

QY 247 FLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPRREQVNSTY 306

DB 117 FIIPKPKDPTLMISRTPEVTCVVDVSDQDDPEVQETWYINNEQVTRTARPLREQQFNSTI 176

QY 307 RVSVSLTVLQDLWNGKEKCKVSNKALPAPTEKTSKAKGQPREPQVYTLPPSREMTK 366

DB 177 RVSVSLTVLQDLWNGKEKCKVSNKALPAPTEKTSKARGQPLEKPKVYTMGPPRELSS 236

QY 367 NOVSLTCLVKGYFSPDAIVAEWESNGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG 426

DB 237 RSVSLTCLVKGYFSPDAIVAEWESNGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG 296

QY 427 NVFSCSVHVEALHNHYTQKSLSLSPGK 453

DB 297 DVFTCSVMHEALHNHYTQKSLSLSPGK 323

RESULT 5

GC2_CAVPO

ID GC2_CAVPO STANDARD: PRT: 329 AA.

AC P01862;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-2 chain C region.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE OF 1-3.

RA Trischmann T.M.;

RL Submitted (APR-1975) to the PIR data bank.

RN [2]

RP SEQUENCE OF 4-68.

RX MEDLINE=71058471; PubMed=55386606;

RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;

RT "Structure of heavy chain from strain 13 guinea pig

RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the

RT half-cysteine joining heavy and light chains.";

RL Biochemistry 10:18-25(1971).

RN [3]

RP SEQUENCE OF 69-133 AND 312-329.

RX MEDLINE=71058486; PubMed=5538616;

RA Turner K.J., Cebra J.J.;

RT "Structure of heavy chain from strain 13 guinea pig

RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal

RT and hinge region cyanogen bromide fragments.";

RL Biochemistry 10:9-17(1971).

RN [4]

RP SEQUENCE OF 134-226.

RX MEDLINE=75036072; PubMed=4429665;

RA Tracey D.E., Cebra J.J.;

RT "Primary structure of the CH2 homology region from guinea pig IgG2

RT antibodies.";

RL Biochemistry 13:4796-4803(1974).

RN [5]

RP SEQUENCE OF 227-311.

RX MEDLINE=75036073; PubMed=4609467;

RA Trischmann T.M., Cebra J.J.;

RT "Primary structure of the CH3 homology region from guinea pig IgG2

RT antibodies.";

RL Biochemistry 13:4804-4811(1974).

RN [6]

RP DISULFIDE BONDS.

RX MEDLINE=71058474; PubMed=4922544;

RA Oliveira B., Lamm M.E.;

RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";

RL Biochemistry 10:26-31(1971).

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN

CC 13 INBRED GUINEA PIGS.

CC PIR: A94553; G2GP.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00407; Igcl; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.


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FT VARIANT 126 127 QV -> EB (IN ZUC).
FT FT /FTID=VAR_003890.
FT VARIANT 134 134 P -> L (IN OMW).
FT FT /FTID=VAR_003891.
FT VARIANT 139 139 F -> Y (IN OMW).
FT FT /FTID=VAR_003892.
FT VARIANT 182 182 T -> A (IN OMW).
FT FT /FTID=VAR_003893.
FT VARIANT 227 227 S -> N (IN OMW).
FT FT /FTID=VAR_003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT FT /FTID=VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMW).
FT FT /FTID=VAR_003896.
FT SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 47.8%; Score 1162; DB 1; Length 290;
Best Local Similarity 91.4%; Pred. No. 8.e-73;
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 222 EPKCDKTHCPAPPELLGSPVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKF 281
DB 59 EPKSCDTPPCPCAPPELLGSPVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVQF 118

QY 282 NWTVDGVEVHNATKPREQYNTYRVVSVTLVHODWLNKGYCKVSKNALPAPIEKT 341
DB 119 KWTVDGVQVHNATKPREQYNTYRVVSVTLVHODWLNKGYCKVSKNALPAPIEKT 178

QY 342 ISKAKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIADVESNGOPENNYKTP 401
DB 179 ISKAGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIADVESNGOPENNYKTP 238

QY 402 PVLDSGSEFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 453
DB 239 PMLDSGSEFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 290

RESULT 7
GCL_MOUSE
ID GCL_MOUSE STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176
SQ SEQUENCE 326 AA; 35946 MW; Q13BAB45EF49B9DA CRC64;

Query Match 47.3%; Score 1150; DB 1; Length 326;
Best Local Similarity 64.0%; Pred. No. 6.7e-72;
Matches 210; Conservative 51; Mismatches 57; Indels 10; Gaps 4;

QY 129 PSVFPLAPSKSTSGGTAALGCLVKDYFPEPVVSWNSGALTSGVHTFPAVLQSSGLYSL 188
DB 6 PSVYPLAPGALKASNSMTLGLCKVGFPEPVVSWNSGALTSGVHTFPAVLQ-SGLYTL 64

QY 189 SSVVTPSSSLGTQTYICNVNHNKPSKTKVDKPKCKDTHCTCPAPPELLGG--PS 245
DB 65 TSSVTVPSSWTPSTVTCNVAHPASSTKVDKVIYPRNCG--GCKPC-----ICTGSEVSS 118

QY 246 VLFPPPKPKDMLISRTPEVTCVVDVSHEDPEVKFNMYDGVHNAKTKPREEQNST 305
DB 119 VFIPPPKPKDVLITLTPKVTGVVDISQDDPEVHFSEWFDVDDVEVHTAQTRPPEQFNST 178

QY 306 YRVSVTLVHODWLNKGYCKVSKNALPAPIEKTISKAKGQPREPOVYTLPPSREMT 365
DB 179 FRYSSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTIKPEGRQVPHVVTMSPTKEMT 238

QY 366 KNOVSLTCLVKGFPSPDIADVESNGOPENNYKTPPVLDSGSEFLYSKLTVDKSRWQ 425
DB 239 QNEVSIITCKMVGFPDPIYVEWMQNGOPOENKTPPTMDTDGGSFYFLSKLVNKKRWQ 298

QY 426 GNVFSCVMHEALHNHYTKSLSPGK 453
DB 299 GNTFTCSVLHEGLHNHTEKSLSPGK 326

RESULT 8
GCL_MOUSE
ID GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).

```

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RX MEDLINE=78242288; PubMed=98524;
RA Aetudbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RL murine myeloma gammal chain.";
RJ J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC . IsoId=P01868-1; Sequence=Displayed;
CC . Note=May be the major isoform;
CC Name=Membrane-bound;
CC . IsoId=P01869-1; Sequence=External;
CC -----
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; G1MS.
DR PDB; 1IGC; 03-JUN-95.
DR GlycoSuiteDB; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 174
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT FTID=CAR_000055.
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
FT SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
Query Match 47.08; Score 1142; DB 1; Length 324;
Best Local Similarity 63.08; Pred. No. 2.4e-71;
Matches 206; Conservative 54; Mismatches 57; Indels 10; Gaps 4;
QY 129 PSVPLAPSKSSTGGTAAIGCLVKDYFPPEVTVSNWNSGALTSGVHTFPAVLQSSGLYSL 188
DB 6 PSVYPLAPGAAQTNSMTVLGCLVKGYFPPEVTVSNWNSGSLSGVHTFPAVLQSD-LYTL 64

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QY 189 SSVVTPSSSLGHTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPP--CPAPELLGGPSV 246
DB ||||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 65 SSVVTPSSPRPSETVTCNVAHFASSTKVKDKIVPRDCG----CKPICITVPEV---SSV 117
DB ||||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 247 FLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVEVHNKATKPRREQYNSTY 306
DB ||||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 118 FIFPKPKDVLTLTPKVTCCVVVDISKDPEVQFSWFDVDVEVHTAQTPREEQFNSTF 177
DB ||||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 307 RVYSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRREMTK 366
DB ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 178 RSVSELPIMHODWLNKGKFKCRVNSAFAFPAPIEKTISKTKGRKPAQOVYTIIPPKQOMAK 237
DB ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 367 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKITVDKSRWQQG 426
DB :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 238 DKVSLTCTMITDFPEDIIVIEWQWNGQPAENYKNTQPIIMNTNGSVFVYKLVNWKSNWEAG 297
QY 427 NVFSCSVMHREALNHYTQKSLSPGK 453
DB ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 298 NTFCTSVLHREGLNHHHTKSLSHSPGK 324
DB ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
RESULT 9
GC3_MOUSE STANDARD; PRT; 329 AA.
ID GC3_MOUSE AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C' region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
Query Match 47.08; Score 1142; DB 1; Length 329;
Best Local Similarity 65.18; Pred. No. 2.4e-71;
Matches 213; Conservative 44; Mismatches 66; Indels 4; Gaps 3;
QY 129 PSVPLAPSKSSTGGTAAIGCLVKDYFPPEVTVSNWNSGALTSGVHTFPAVLQSSGLYSL 188

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Search completed: August 12, 2003, 16:30:28
Job time : 14.152 secs

| Result No. | Query | Score | Match | | Length | DB | ID | Description |
|------------|--------|-------|-------|----|--------|----|--------|--------------|
| | | | Match | % | | | | |
| 1 | 2201.5 | 80.5 | 471 | 4 | Q8TC77 | | Q8tc77 | homo sapien |
| 2 | 2201.5 | 93.0 | 521 | 4 | Q8N4Y9 | | Q8n4y9 | homo sapien |
| 3 | 1903 | 78.2 | 473 | 4 | Q8TC63 | | Q8tc63 | homo sapien |
| 4 | 1611.5 | 66.3 | 509 | 4 | Q8NF17 | | Q8nf17 | homo sapien |
| 5 | 1552.5 | 63.8 | 469 | 11 | Q8R3V9 | | Q8r3v9 | mus musculus |
| 6 | 1511.5 | 62.2 | 437 | 11 | Q9RIA4 | | Q9ria4 | mus musculus |
| 7 | 1469.5 | 60.4 | 463 | 11 | Q9YLC4 | | Q9ylc4 | mus musculus |
| 8 | 1463.5 | 59.2 | 473 | 11 | Q91Z05 | | Q91z05 | mus musculus |
| 9 | 1450.5 | 59.6 | 473 | 11 | Q9D8L4 | | Q9d8l4 | mus musculus |
| 10 | 1424 | 58.6 | 468 | 11 | Q9DL84 | | Q9dl84 | mus musculus |
| 11 | 1423.5 | 58.5 | 473 | 11 | Q99L25 | | Q99l31 | mus musculus |
| 12 | 1371 | 56.4 | 474 | 11 | Q8R3H6 | | Q8r3h6 | mus musculus |
| 13 | 1258 | 51.7 | 701 | 4 | Q96PQ8 | | Q96pq8 | homo sapien |
| 14 | 1249.5 | 51.4 | 337 | 6 | Q95M34 | | Q95m34 | equus caball |
| 15 | 875.5 | 36.0 | 597 | 4 | Q96BB9 | | Q96bb9 | homo sapien |
| 16 | 872 | 35.9 | 613 | 4 | Q8WUK1 | | Q8wuk1 | homo sapien |

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QY 119 VSSASTKKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 VSSAST--KGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 196
QY 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTTCPCPCAP 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTTCPCPCAP 256
QY 239 ELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKATKPR 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 ELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKATKPR 316
QY 299 EQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLP 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 EQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLP 376
QY 359 PSREEMTKNOVSLTCLVKGFFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 PSREELTKNOVSLTCLVKGFFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 436
QY 419 DKSRWQOQGNVFCSCVMHEALHNHYTKQSLSLSPGK 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 DKSRWQOQGNVFCSCVMHEALHNHYTKQSLSLSPGK 471

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RESULT 2

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Q8N4Y9 ID Q8N4Y9 PRELIMINARY: PRT: 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC033178; AAH33178.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00407; Igc1. 3.
DR SMART: SM00406; IGV. 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

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Query Match 83.0%; Score 2019.5; DB 4; Length 521;
Best Local Similarity 77.2%; Pred. No. 1.3e-160;
Matches 390; Conservative 23; Mismatches 37; Indels 55; Gaps 5;
QY 1 EVQLVESGGGLVQPGGSLRLSCAAGYSSITSGYSWNMTIROAPGKLEWNA---SITYDGS 57
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVQLVDSGGGLVQPGGSLRLSCAAGFYIVSHYV-EWVRQAPGKGPVWGCFRKAHKST 78
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 58 TNYADSVKGRFTISRDDSKNTFTYIQMNSLR AEDTAVYICARGSHYFG--HWHEAVWGQGT 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 TEYAASVKGRFTILRDSKNSVHLQMSLTKTDDTAVYVCVRDLGEGACKYDWFYDIWGRGI 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 LVTYSSASTKKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 175
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 LVTYSSAST--KGPSVFLPAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 196
QY 176 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTTCPCAP 221
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 197 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTTCPCAP 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 222 -----EPKSCDKTTCPCAPPELLGGPSVFL 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 RCPEPKSCDTTPPCPCPEPKSCDTTPPCPCPEPKSCDTTPPCPCPEPKSCDTTPPCPCPE 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 249 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKATKPREEQYNSTYRV 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNKATKPREEQYNSTYRV 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 309 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSPREEEMTKNQ 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSPREEEMTKNQ 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 369 VSLTCLVKGFFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQOQGNV 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 VSLTCLVKGFFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQOQGNV 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 429 FSCSYMHEALHNHYTKQSLSLSPGK 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 497 FSCSYMHEALHNHYTKQSLSLSPGK 521

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RESULT 3

```

Q8TC63 ID Q8TC63 PRELIMINARY: PRT: 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC025985; AAH25985.1; -.
DR InterPro: IPR000923; BlueCu1.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IGV. 1.
DR PROSITE: PS00196; COPPER_BLUE; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

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Query Match 78.2%; Score 1903; DB 4; Length 473;
Best Local Similarity 80.4%; Pred. No. 6.4e-151;
Matches 364; Conservative 33; Mismatches 48; Indels 8; Gaps 4;
QY 2 VQLVESGGGLVQPGGSLRLSCAAGYSITSGYSWNMTIROAPGKLEWASITVDGSTNY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 LQLESFGPLLPKPSVTLSTCTVSGDSVASSSYTWGVRQPPGKGLWIGTIFNSGNMY 87
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ADSYKGRFTISRDDSKNTFTYIQMNSLR AEDTAVYICARGSHYFGHWIFAVWGQGTTLVTS 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 88 SPSLRSRVNTSADMSENSEFYLKLDVTAADTAVYICAAAGHLVWFG--AHWGQGLVSVS 145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 SASTKKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 PAST--KGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTTCPCAP 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTTCPCAP 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT. T 5

| | | | | | |
|--------|--------------|------------------|--------|-------------------------|------|
| | RESULT | 5 | PRT; | 469 | AA.. |
| Q8R3V9 | PRELIMINARY; | ID | Q8R3V9 | | |
| AC | Q8R3V9: | | | | |
| DT | 01-JUN-2002 | (TREMBLrel. | 21, | Created) | |
| DD | 01-JUN-2002 | (TREMBLrel. | 21, | Last sequence update) | |
| DE | 01-MAR-2003 | (TREMBLrel. | 23, | Last annotation update) | |
| DG | Hypothetical | 52.0 kDa protein | | | |

NCBI TaxID=10090;
[1]
SEQUENCE FROM N. A.
Strausberg P.;
RA
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RL
EMBL: BC024405; RAH24405.1; -
DR

DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS0835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypoethetical protein

DR PROSITE: PS00050; IG_LIRAL, 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F15D05457 CRC64;
Query Match 63.8%; Score 1552.5; DB 11; Length 469;
Best Local Similarity 63.3%; Pred NO. 1.5e-121;

| | | | | | | | | |
|----|-----|---|-----|-------------|----|--------|-----|------|
| | 227 | CONSERVATIVE | 69 | HISMACTACTG | 68 | AACAGC | 157 | CAGS |
| Qy | 1 | EVLVESGGGLVPQGSLRLSCAVSGYSITSGYSHNWIRQAPGKLEWASITYDG--- | \$ | 57 | | | | |
| | | | | | : | | | : |
| Dd | 20 | EVLNVESSGGLVPQGSLRLSCAASGFTTDT-YMSWVRPPGKALEWLGFINKANGYT | 78 | | | | | |
| | | | | | | | | |
| Qy | 58 | TNYADSVKGRFTISRDSKNFTYLOMNSLRAEDTAETAYCA---RGSYFGHWHIFAVWGQ | 114 | | | | | |
| | | : | | | | | | |
| Dd | 79 | TEYSASVKGRFTISRDNQSILYLQMNALRAEDSATYYCARDRRSYYYSGTSFAVWGQ | 138 | | | | | |

QY
113 TLTVSSGKGRQSVLEAFPSNSLSQGLRGLKGLRLEPEPVTVMNSGSLSSGVH 176
|||||:| |||:||||:|: ||||| |||||:||||:|:||||
139 TLTVSSAQT--TPPSVYPLAPGSAQNTNSMVTLGCLKGYEPEPVTVTWNSGSLSSGVH 196

D_b 197 TFFAVLQSD-LYTLSSVTVPSSWTWPSQTVTCTNVAHPASTKVKDKKIVPRDCG-----CKP 251

D0 252 CICTVPEV--SSVFIFPKPKDVLITLTPKVTCVVVDISKDDPEVQFSNEVDDEVHT 308

[illegible]

QY
355 QVILPPKREEMINQVSUICLVAGIFPSULAVENSGQGENNIALIFFVUDSDGSFFL 418
||||| : : : ||||| : : | : ||| ||| : ||| : ||| :
369 QVVTIPPKREQMADKVSLTCMITDFPFPITVEWQNGQPAENKYNTQPMIDTDSGYFV 428

Dd

[illegible]

RESULT 6

Q9RIA4 PRELIMINARY; PRT; 437 AA.
 AC Q9RIA4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Gammal heavy chain of Mab7 (Fragment).
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003435; AAH03435.1;
 DR HSSP: P01842; 7FAB.
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00406; Igv; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 FT NON_TER 1
 FT TER 437
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match

Best Local Similarity 62.2%; Score 1511.5; DB 11; Length 437;

Matches 282; Conservative 70; Mismatches 83; Indels 19; Gaps 7;

QY 2 VOLVESGGGLVQPGSLRLSCAVSGYISGYSNNIRQAPGKGLWVASITPDGSTNYA 61
 DB 1 VOLVESGGGLVQPGSLRLSCAVSGYISGYSNNIRQAPGKGLWVASITPDGSTNYA 61
 QY 62 DSVKGRFTISRDSSKNTFYIOMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 121
 DB 62 DSVKGRFTISRDSSKNTFYIOMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTS 121
 QY 60 DSVKGRFTIYKDKRNLISLQMSLRSEDSTAMTCARGD-----YSAYMGPGTLTVSA 113
 DB 60 DSVKGRFTIYKDKRNLISLQMSLRSEDSTAMTCARGD-----YSAYMGPGTLTVSA 113
 QY 122 ASTKGGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 181
 DB 114 AKT--TPPSVYPLAPGSAQTNSMVTLCGLVKGYFPEPTVSNVNSGALTSGVHTFPAVLQ 171
 QY 182 SSGLYSLSSVTVPSSTSLGTQTYICNVNHPKSNWKVDKVEPKSCDKTHTCPP--CPAPE 239
 DB 172 SD-LYTLSSSVTVPSSTSLGTQTYICNVNHPKSNWKVDKVEPKSCDKTHTCPP--CPAPE 239
 QY 240 LLGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPRE 299
 DB 227 V---SSVFIPLPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPRE 299
 QY 300 EQYNSTYRVVSVTLVHQLWLNKKEYCKVSKNKAAPAPAEKTIKSKAKGPREPOVYTLPP 359
 DB 284 EGFNSTFRSVSELPIMHQDLWLNKKEYCKVSKNKAAPAPAEKTIKSKAKGPREPOVYTLPP 343
 QY 360 SREEMTKNOVSLTCLVKGYPSDIAVWESNGQPNENYKTPPVLDSDGSFFLYSKLTV 419
 DB 344 PREQMAKDVSLTCLVKGYPSDIAVWESNGQPNENYKTPPVLDSDGSFFLYSKLTV 419
 QY 420 KSRWQGNVFCSSVMHEALHNYTKSLSPCK 453
 DB 404 KSNWEAGNFTCSVLHLEGLNHHHTKSLSPCK 437

RESULT 7

Q99LC4

Q99LC4 PRELIMINARY; PRT; 463 AA.
 AC Q99LC4
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1810060009 gene.
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003435; AAH03435.1;
 DR HSSP: P01842; 7FAB.
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00406; Igv; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 60.4%; Score 1469.5; DB 11; Length 463;
 Best Local Similarity 60.0%; Pred. No. 1.3e-114;
 Matches 274; Conservative 77; Mismatches 89; Indels 17; Gaps 9;

QY 1 EVLVESGGGLVQPGSLRLSCAVSGYISGYSNNIRQAPGKGLWVASITPDGSTN- 59
 DB 20 QVQLQQSGAELARPGASVRLSCKASGYTFT-GYGVSWVKORTGGLWVGELI-YPGSGNT 77
 QY 60 -YADSVKGRFTISRDSSKNTFYIOMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTV 118
 DB 78 YYSKFKGKATLTDKSSSTAYMHLSSLTSEDSAVYFCARSS-YYSYDLFAVWGQGLTV 136
 QY 119 VSSASTKGGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPA 178
 DB 137 VSAAKT--TPPSVYPLAPGSAQTNSMVTLCGLVKGYFPEPTVSNVNSGALTSGVHTFPA 194
 QY 179 VLQSSGLYSLSSVTVPSSTSLGTQTYICNVNHPKSNWKVDKVEPKSCDKTHTCPP--CP 236
 DB 195 VLQSD-LYTLSSSVTVPSSTSLGTQTYICNVNHPKSNWKVDKVEPKSCDKTHTCPP--CP 249
 QY 237 APQLLGGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 296
 DB 250 VPEV---SSVFIPLPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 306
 QY 297 PREEQYNSTYRVVSVTLVHQLWLNKKEYCKVSKNKAAPAPAEKTIKSKAKGPREPOVY 356
 DB 307 PREEQYNSTFRSVSELPIMHQDLWLNKKEYCKVSKNKAAPAPAEKTIKSKAKGPREPOVY 366
 QY 357 LPSSREEMTKNOVSLTCLVKGYPSDIAVWESNGQPNENYKTPPVLDSDGSFFLYSKL 416
 DB 367 IPPPEQMAKDVSLTCLVKGYPSDIAVWESNGQPNENYKTPPVLDSDGSFFLYSKL 426
 QY 417 TVDKSRWQGNVFCSSVMHEALHNYTKSLSPCK 453
 DB 427 NVQKSNWEAGNFTCSVLHLEGLNHHHTKSLSPCK 463

RESULT 8
 Q91Z05 PRELIMINARY; PRT; 473 AA.
 AC Q91Z05
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 51.9 kDa protein.
 GN AU044919.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AHA10327.1; -.
DR MGD; MGI:2144967; A0044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 60.2%; Score 1463.5; DB 11; Length 473;
Best Local Similarity 61.8%; Pred. No. 4.2e-114;
Matches 286; Conservative 62; Mismatches 95; Indels 21; Gaps 9;

QY 1 EVLVESGGGLVOPGGSLRSCAVSGYSITSGYSNWIRQAPGKGLEWVASITYDGSN- 59
Db 20 EVLVESGGGLVOPGGSLRSCAVSGFTF-SDYGMHWVQAPGKGLEWVAYIN-SGSTTI 77
QY 60 -YADSVKGRFTISRDSKNTFYIQMNSLRADPAVYVCARGSHYFGHW--HFAVWGQGT 116
Db 78 YYADVTKGRFTISRDNKNTFLQMTSLRSEDPAVYVCAREL-----WLRIDYWGQGT 132
QY 117 VTSSASTKGGPSVPLAPSSKSTSGGTAALGCLVKDYKPEPVTVSWNSGALTSGVHTF 176
Db 133 ITVSSAKT--TPPSVYPLAPCGDGTGSSVTLGCLVKGYFPEPVTVTWNSGSLSSVHTF 190
QY 177 PAVLQSGGLYSLSSVTVPSSSLTGTQTYICNVNHPKSNTKVDKKVPEPKSCKDKH-HPCPP- 234
Db 191 PALLO- SGLYTMSSSVTVPSSTQVTVCSVAHPASSITVDKKLEPGSGFISTINCPPC 249
QY 235 -----CPAPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGE 289
Db 250 KECHKCAPNLEGGPSVFIPPPNIKDVLMISLTSLKPKVTCVVVDVSEDDPDQVSWFVNNVE 309
QY 290 VHNAKTKPREEQYNSTYRVVSVLTVLHDWLNKGKVKCKVSNKALPAPIEKTISKAKGQP 349
Db 310 VHTAQVQTHREDYNTIRVVSALPIQHDWMSGRFKCKVNNKDLPSPIERTISKINGLV 369
QY 350 REPQVTLPPSREEMTKNOVSLTCLVKGYFSPDIAEVESNGOPENNYKTTTPVLDSDGS 409
Db 370 RAPQVILPPAPQLSRKDVSLTCLVGFNPGDISVEWTSNTEENYKDTAPVLDSDGS 429
QY 410 FFLYSLKLVKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
Db 430 YFTYSKLDIKTSKWEKTSFSCNVREHGLKNLYLKKTKISRSCK 473

RESULT 9
Q9DBL4
ID Q9DBL4 PRELIMINARY; PRT; 473 AA.
AC Q9DBL4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1810060009RIK protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:585-590(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475PBB CRC64;

Query Match 59.6%; Score 1450.5; DB 11; Length 473;
Best Local Similarity 59.6%; Pred. No. 5.2e-113;
Matches 274; Conservative 74; Mismatches 99; Indels 13; Gaps 7;

QY 1 EVLVESGGGLVOPGGSLRSCAVSGYSITSGYSNWIRQAPGKGLEWVASI-TYDGSN 59
Db 20 QVLQSGGLVOPGGSLRSCAVSGFTF-SDYGMHWVQAPGKGLEWVAYIN-SGSTTI 78
QY 60 YADSVKGRFTISRDSKNTFYIQMNSLRADPAVYVCARGSHYFGHWFAVWGQGT 119
Db 79 YNEKEGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR-SGYDYDFAVWGQGT 136
QY 120 SSASTKGGPSVPLAPSSKSTSGGTAALGCLVKDYKPEPVTVSWNSGALTSGVHTP 179
Db 137 SAAKT--TAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSVHT 194
QY 180 LQSSGLYSLSSVTVPSSSLTGTQTYICNVNHPKSNTKVDKKVPEK-----SCDK 233
Db 195 LQ-SGLYTLSSVTVTSNTWPSQTITCNVAHPASSITKVDKIEPRVITQNPCLP 253
QY 234 PCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDG 293
Db 254 PCAAPDLGGPSVFIPPPKIDVLMISLSPNVCVVVDVSEDDPDQVSWFVNNVEHT 313
QY 294 KTKPREEQYNSTYRVVSVLTVLHDWLNKGKVKCKVSNKALPAPIEKTISKAKG 353
Db 314 QTQTHREDYNTLRVVSALPIQHDWMSGRFKCKVNNRALSPIEKTISKPRGVP 373
QY 354 VYTLPPSREEMTKNOVSLTCLVKGYFSPDIAEVESNGOPENNYKTTTPVLDSDG 413
Db 374 VYVLPPEAEEMTKFSLTCMTITGFLPAEIAVDMTSGRTQYKNTATVLDSDGS 433
QY 414 SKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
Db 434 SKLRVQKSTWERSLFCVSVVHGLNHLTKTISRSLGK 473

RESULT 10

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00406; Igv_1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00835; IG-LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match          56.4%; Score 1371; DB 11; Length 474;
Best Local Similarity 57.1%; Pred. No. 2.4e-106;
Matches 264; Conservative 74; Mismatches 108; Indels 16; Gaps 8;

QY 1 EVQLVESGGGLVQPGSLRLCAVSGYSITTSYGSW-NWIRQAPGKGLEWVASI-TYDGT 58
Db 20 QVQLLQSGPELVKPGASVKISCRASGYAFSK--SWNNWVKRPGKLEWIGRIFFCDGDT 77

QY 59 NYADSVKGRFTISRDDSKNTFYLQNNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLVT 118
Db 78 HYSGRFQGRKAKLTADKSSVTAFLQLTSLTSEDSAVYFCARDSDYGD--YFDDWGQCATVT 135

QY 119 VSSASTKCKGKPSVEPLAPSSKTSSTGTAALGCLVXDYFPEPTVSNNSGALTSGVHTFPA 178
Db 136 VSSAKT--TPPSVYPLAPCGDGTGSSVTLGCLVKGYPFPEPTVSNNSGSSVHTFPA 193

QY 179 VLQSGSLYSLSWVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKT--HTCPP--- 234
Db 194 LIQ-SGLYTMSSSVVTPSTWFSQIVTCSVAHPASTTVDKLESGPISTINPCPPCKE 252

QY 235 ---CPAPELLGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 291
Db 253 CHKCAPNLEGSPSVEIRPNKIDVLMISLTPKVCVVVDSEDDPDVQISFWNVNVEVH 312

QY 292 NAKTPREEQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIETKISKAKQPRE 351
Db 313 TAQQTTHREDYNTSRVVSALPIQHDWMSGFEKCKVNNKDLPSPIERTISKIRGLVRA 372

QY 352 PQVYTLPPSREEMTKNOVSLTCLVKGFPSPDIKAVESNGQPNENYKTPPVLDSDSGSPF 411
Db 373 PQVYILPPAEQLSRKDSLTCLVGFNPGDISVEMTSNGHTEENYKDTAPVLDSDSGSYF 432

QY 412 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 453
Db 433 IYSKLDIKTSKEKTDSEFCNVRHEGLKNLYLKTKTSRSPGK 474

RESULT 13
Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Factor VII active site mutant immunocongulate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RU Hu Z.; Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF272774; AAK58686.1; -.
DR HSP: P00761; 1AN1.
DR InterPro: IPR00152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.

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DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00047; ig; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00407; IGC1; 1.
DR SMART: SM00020; trypt_spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00835; IG-LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match          51.7%; Score 1258; DB 4; Length 701;
Best Local Similarity 81.7%; Pred. No. 1.2e-96;
Matches 241; Conservative 6; Mismatches 30; Indels 18; Gaps 3;

QY 162 VSNNSGALTSVHTFPAVLQSSGLYSLSVSVTVPPSSSLGTQTYICNVNHNKPS---NTKVD 218
Db 422 VSNQGQCATVG-----HFGVY-----TVSQYIEWLQKLMSEPRPGVLLRAPFP 466

QY 219 KKEVPKSCDKTHTCPCPAPELGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPE 278
Db 467 GSAEPKSCDKTHTCPCPAPELGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPE 526

QY 279 VKFNWYVDGVEVHNAKTKPREQYNSTYRVSVSVTLVTLHODWLNKGEYKCKVSNKALPAPI 338
Db 527 VKFNWYVDGVEVHNAKTKPREQYNSTYRVSVSVTLVTLHODWLNKGEYKCKVSNKALPAPI 586

QY 339 EKTISKAKGQPREPVYTLPPSREEMTKNOVSLTCLVKGFPSPDIKAVESNGQPNENYK 398
Db 587 EKTISKAKGQPREPVYTLPPSREEMTKNOVSLTCLVKGFPSPDIKAVESNGQPNENYK 646

QY 399 TTPPVLDSDSGSFELYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 453
Db 647 TTPPVLDSDSGSFELYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 701

RESULT 14
Q95M34 PRELIMINARY; PRT; 337 AA.
ID Q95M34;
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (fragment).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RU Wagner B.;

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Search completed: August 12, 2003, 16:31:42
Job time : 47.2325 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:17:47 ; Search time 25.6662 seconds
(without alignments)
1348.171 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGRVT.....EVTHQGLSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------------|
| 1 | 1135 | 100.0 | 218 | 20 | AAW95658 Mus musculus anti- |
| 2 | 1135 | 100.0 | 218 | 21 | AAW85200 Light chain amino |
| 3 | 1135 | 100.0 | 218 | 22 | AAW76947 Full variable ligh |
| 4 | 1128 | 99.4 | 218 | 14 | AAW33312 Humanised MaE11 ve |
| 5 | 1112 | 98.0 | 218 | 20 | AAV50030 Human E27 anti-IgE |
| 6 | 1112 | 98.0 | 218 | 20 | AAW95660 Mus musculus anti- |
| 7 | 1112 | 98.0 | 218 | 20 | AAW95662 Mus musculus anti- |
| 8 | 1112 | 98.0 | 218 | 21 | AAW07472 Amino acid sequenc |
| 9 | 1112 | 98.0 | 218 | 22 | AAW74211 E27 anti-IgE antib |

| | | | | | |
|----|--------|------|-----|----|-----------------------------|
| 10 | 1109 | 97.7 | 218 | 20 | AAW95669 Mus musculus anti- |
| 11 | 1109 | 97.7 | 218 | 20 | AAW95664 Mus musculus anti- |
| 12 | 1109 | 97.7 | 218 | 22 | AAW7087 Anti-IgE antibody, |
| 13 | 1109 | 97.7 | 218 | 22 | AAW76949 Full length light |
| 14 | 1109 | 97.7 | 218 | 22 | AAW76951 Full length light |
| 15 | 1109 | 97.7 | 218 | 22 | AAW76953 Variable light cha |
| 16 | 1109 | 97.7 | 218 | 22 | AAW76958 Humanised anti-L-s |
| 17 | 1108 | 97.6 | 218 | 18 | AAW13563 Humanised anti-Fas |
| 18 | 1100 | 96.9 | 238 | 21 | AAW90930 Humanised anti-Fas |
| 19 | 1100 | 96.9 | 238 | 23 | ABW74899 Humanised anti-Fas |
| 20 | 1099 | 96.8 | 238 | 21 | AAW90932 Humanised anti-Fas |
| 21 | 1099 | 96.8 | 238 | 23 | ABW74901 Humanised anti-Fas |
| 22 | 1096 | 96.6 | 238 | 21 | AAW90931 Humanised anti-Fas |
| 23 | 1096 | 96.6 | 238 | 23 | ABW74900 Humanised anti-Fas |
| 24 | 1036 | 91.3 | 214 | 21 | AAV93735 The kappa chain of |
| 25 | 1036 | 91.3 | 238 | 19 | AAW83034 Anti-Fas humanised |
| 26 | 1036 | 91.3 | 238 | 21 | AAW14777 Humanised anti-Fas |
| 27 | 1036 | 91.3 | 238 | 21 | AAW90927 Humanised HFE7A de |
| 28 | 1036 | 91.3 | 238 | 23 | ABW74896 Humanised anti-Fas |
| 29 | 1036 | 91.3 | 238 | 23 | ABW74942 Humanised anti-Fas |
| 30 | 1031.5 | 90.9 | 237 | 21 | AAV96298 Human IGFAM-10 imm |
| 31 | 1031 | 90.8 | 238 | 19 | AAW83031 Anti-Fas humanised |
| 32 | 1031 | 90.8 | 238 | 21 | AAW14772 Humanised anti-Fas |
| 33 | 1031 | 90.8 | 238 | 21 | AAW90922 Humanised anti-Fas |
| 34 | 1031 | 90.8 | 238 | 23 | ABW74891 Humanised anti-Fas |
| 35 | 1031 | 90.8 | 238 | 23 | ABW74937 Humanised anti-Fas |
| 36 | 1028 | 90.6 | 240 | 24 | ABJ38594 Hepatitis C virus |
| 37 | 1027.5 | 90.5 | 237 | 21 | AAV96289 Human IGFAM-1 immu |
| 38 | 1026 | 90.4 | 260 | 23 | ABP41164 Human ovarian anti |
| 39 | 1024 | 90.2 | 240 | 24 | ABJ38595 Hepatitis C virus |
| 40 | 1019.5 | 89.8 | 237 | 21 | AAV96301 Human IGFAM-13 imm |
| 41 | 1018 | 89.7 | 238 | 19 | AAW83032 Anti-Fas humanised |
| 42 | 1018 | 89.7 | 238 | 21 | AAW14773 Humanised anti-Fas |
| 43 | 1018 | 89.7 | 238 | 21 | AAW90923 Humanised anti-Fas |
| 44 | 1018 | 89.7 | 238 | 23 | ABW74892 Humanised anti-Fas |
| 45 | 1018 | 89.7 | 238 | 23 | ABW74936 Humanised anti-Fas |

ALIGNMENTS

RESULT 1
AAW95658
ID AAW95658 standard; protein; 218 AA.
XX
AC AAW95658;
XX
DT 08-JUN-1999 (first entry)
XX
Mus musculus anti-IgE e25 full length variable light chain.
XX
Variable light chain; IgE: antibody; anti-IgE: reduction; prevention;
XX
histamine; production; IgE: hypersensitivity; allergen; anaphylaxis;
KW
atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW
eczema; anaphylactic shock; urticaria.
OS
Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-USI3410.
XX
PR 02-JUL-1997; 97US-0887352.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Lowe J, Lowman HB, Presta LG;
XX
DR WPI; 1999-106057/09.
XX
PT Improving affinity of polypeptides, particularly anti-IgE antibodies

DR WPI: 2001-122353/13.
 XX
 PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phase display -
 XX
 PS Disclosure: Fig 2: 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody
 CC with improved anti-IgE antibody activity. The antibody has improved
 CC action due to a process comprising, a) identifying aspartyl residues
 CC prone to isomerization in unimproved anti-IgE (immunoglobulin E)
 CC antibody; b) substituting alternative residues to create candidate
 CC molecules, and c) selecting those candidate molecules which display
 CC affinity against the target molecule. Use of the antibody results in
 CC antiasthmatic; antiallergic; ophthalmological; dermatological and
 CC antiinflammatory activity. The antibodies are useful for treating
 CC IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
 CC eczema, urticaria and food allergies. The mutant antibodies produced by
 CC the above mentioned nucleic acids may also be used as affinity
 CC purification agents and in diagnostic assays for detecting the expression
 CC of an antigen of interest in specific cell, tissues or serum. Amino acid
 CC sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of
 CC the invention. Polynucleotide sequence AAF69253 represents an expression
 CC plasmid used in the course of the invention, and oligonucleotides
 CC AAF69254 - AAF69271 are used in the generation of affinity improved
 CC anti-IgE antibodies.
 XX
 SQ Sequence 218 AA;
 Query Match 100.0%; Score 1135; DB 22; Length 218;
 Best Local Similarity 100.0%; Pred. No. 3.1e-57;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYDGMNMYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYDGMNMYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 DB 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IPPSPDEQLKSGTASVCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYSL 180
 DB 121 IPPSPDEQLKSGTASVCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 RESULT 4
 AAR33312
 ID AAR33312 standard; Protein; 218 AA.
 XX
 AC AAR33312;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-JUL-1993 (first entry)
 XX
 DE Humanised MAE11 Version 1 (intact IgG); light chain.
 XX
 KW Antibody; high affinity; FCEH; low affinity; FCEL;
 KW IgE receptor; histamine; mast cell; basophil; Kabat;
 KW CDR; murine; MAE11; Fab; humaeliv1.
 XX
 OS Synthetic.
 XX
 PN WO9304173-A1.
 XX
 PD 04-MAR-1993.
 XX

PF 14-AUG-1992; 92WO-US06860.
 XX
 PR 14-AUG-1991; 91US-0744768.
 PR 07-MAY-1992; 92US-0879495.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 XX WPI: 1993-094004/11.
 DR
 XX Polypeptide(s) binding to specific Fc epsilon receptors - act as
 PT IgE antagonists; useful for treating and preventing IgE-mediated
 PT disorders e.g. allergies
 XX
 PS Example 4; Fig 3; 113pp; English.
 XX
 CC Residues were selected from MAE11 and inserted or substituted into
 CC a human Fab antibody background (Vh region Kabat'subgroup III and V1
 CC region kappa subgroup I). A first version, humaeliv1 or version 1 is
 CC given below. The affinity of version 1 was assayed and found to be
 CC ca. 100 times lower than that of the donor antibody MAE11.
 CC Therefore, further modifications in the sequence of version 1
 CC were made.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 218 AA;
 Query Match 99.4%; Score 1128; DB 14; Length 218;
 Best Local Similarity 99.5%; Pred. No. 7.7e-57;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYDGMNMYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYDGMNMYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 DB 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IPPSPDEQLKSGTASVCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYSL 180
 DB 121 IPPSPDEQLKSGTASVCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 RESULT 5
 AAY50030
 ID AAY50030 standard; protein; 218 AA.
 XX
 AC AAY50030;
 XX
 DT 19-JAN-2000 (first entry)
 XX
 DE Human E27 anti-IgE antibody light chain.
 XX
 KW Immunoglobulin E; IgE; antibody; vascular endothelial growth factor;
 KW VEGF; chimeric; IgG; assay; Fc gamma receptor; low affinity; hexamer;
 KW complex; cross-linked; enzyme-linked immunosorbent assay; ELISA;
 KW light chain.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9951642-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US06858.
 XX

PR 02-APR-1998: 98US-0054255.
 PR 15-JAN-1999: 99US-0116100.

XX (GETH) GENENTECH INC.

XX Idusogie EE, Mulkerrin MG, Presta LG, Shields RL;

XX WPI; 1999-620197/53.

XX Antibody variants useful in receptor binding assays and in therapy of
 PT conditions needing treatment -

PS Example 1; Fig 4A; 69pp; English.

CC This sequence represents human E27 anti-IgE (immunoglobulin E) antibody
 CC light chain, which, along with the E27 heavy chain (AA50031), comprises
 CC the E27 anti-IgE antibody. The E27 antibody binds the constant regions
 CC of IgE, and when mixed with IgE in an equimolar ratio, forms a stable
 CC hexamer consisting of three E27 molecules and 3 IgE molecules. This
 CC complex-forming ability can be utilised in an assay for the binding of
 CC IgG to Fc gamma receptors Fc-gamma-1Ia, Fc-gamma-1Ib and Fc-gamma-1II,
 CC which have IgG affinities in the micromolar range and so cannot be
 CC assayed via a standard ELISA (enzyme-linked immunosorbent assay)
 CC protocol. The low affinity receptor binding assay uses E27 and a
 CC recombinant chimeric form of IgE, consisting of a human IgE Fc region
 CC and the Fab regions of an anti-VEGF (vascular endothelial growth factor)
 CC antibody, which binds two VEGF molecules per mole of anti-VEGF chimeric
 CC IgE. When recombinant human VEGF is added at at 2:1 molar ratio to the
 CC IgE:E27 hexamer complexes, the hexamers are linked into larger complexes
 CC via IgE:Fab:VEGF interactions. The E27 component of this complex binds
 CC to the Fc-gamma-1Ia, Fc-gamma-1Ib and Fc-gamma-1II alpha subunits to
 CC permit detection via ELISA.

XX Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 20; Length 218;
 Best Local Similarity 98.2%; Pred. No. 6.2e-56;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDVRTITCRASKPVDGSDYNNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCQSHEDPTTFGQGTKEIKRTVAAPSVF 120
 DB 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCQSHEDPTTFGQGTKEIKRTVAAPSVF 120
 QY 121 IPPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 DB 121 IPPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 QY 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

AAW95660
 ID AAW95660 standard; protein; 218 AA.

XX AAW95660;

XX 08-JUN-1999 (first entry)

XX Mus musculus anti-IgE e26 full length light chain.

XX Light chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria.
 XX Mus musculus.

PN WO9901556-A2.

XX 14-JAN-1999.

XX 30-JUN-1998; 98WO-US13410.

XX 02-JUL-1997; 97US-0887352.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Lowe J, Lowman HB, Presta LG;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies
 PT - by identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against
 PT the target

XX Disclosure; Pages 94-95; 129pp; English.

XX The sequence is that of the full length light chain of e26. It
 CC was used as part of a method to improve the affinity of anti-IgE
 CC antibodies such as e26 and e27. The e26 and e27 antibodies can
 CC be used for reducing or preventing IgE mediated production of
 CC histamine in a mammal. They can be used for treating a disorder
 CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,
 CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic
 CC shock and urticaria. The antibodies can also be used for affinity
 CC purification, detection and diagnosis.

XX Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 20; Length 218;
 Best Local Similarity 98.2%; Pred. No. 6.2e-56;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDVRTITCRASKPVDGSDYNNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCQSHEDPTTFGQGTKEIKRTVAAPSVF 120
 DB 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCQSHEDPTTFGQGTKEIKRTVAAPSVF 120
 QY 121 IPPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 DB 121 IPPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 QY 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7

AAW95662
 ID AAW95662 standard; protein; 218 AA.

XX AAW95662;

XX 08-JUN-1999 (first entry)

XX Mus musculus anti-IgE e27 full length light chain.

XX Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria.

XX Mus musculus.

XX WO9901556-A2.

PD 14-JAN-1999.
 XX 30-JUN-1998; 98WO-US13410.
 XX 02-JUL-1997; 97US-0887352.
 XX (GETH) GENENTECH INC.
 PA Jardieu PM, Lowe J, Lowman HB, Presta LG;
 XX WPI; 1999-106057/09.
 XX
 XX Improving affinity of polypeptides, particularly anti-IgE antibodies
 PT - by identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against
 PT the target
 XX
 XX Disclosure; Page 97; 129pp; English.
 XX
 XX The sequence is that of the full length heavy chain of e27. It
 CC was used as part of a method to improve the affinity of anti-IgE
 CC antibodies such as e26 and e27. The e26 and e27 antibodies can
 CC be used for reducing or preventing IgE mediated production of
 CC histamine in a mammal. They can be used for treating a disorder
 CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,
 CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic
 CC shock and urticaria. The antibodies can also be used for affinity
 CC purification, detection and diagnosis.
 XX
 SQ Sequence 218 AA;
 Query Match 98.0%; Score 1112; DB 20; Length 218;
 Best Local Similarity 98.2%; Pred. No. 6.2e-56;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSLSASVGDVRVITTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSLSASVGDVRVITTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGTDFLTLTISLQPEDPATYVCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 DB 61 GVPSRFGSGSGTDFLTLTISLQPEDPATYVCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 QY 121 IFPPSDQLKSGTASVVCLLNFPYPRKAYQWKVDNALQSGNSQESVTEQDSKDSYSL 180
 DB 121 IFPPSDQLKSGTASVVCLLNFPYPRKAYQWKVDNALQSGNSQESVTEQDSKDSYSL 180
 QY 181 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
 RESULT 8
 AAB07472
 ID AAB07472 standard; protein; 218 AA.
 AC AAB07472;
 XX 20-OCT-2000 (first entry)
 XX
 XX Amino acid sequence of E27 and anti-IgE antibody light chain.
 DE anti-IgE antibody; light chain; Fc region; effector function; cancer;
 KW allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
 XX
 OS Synthetic.
 XX
 XX W0200042072-A2.
 XX
 XX 20-JUL-2000.
 XX
 XX 14-JAN-2000; 2000WO-US00973.
 PF
 XX

PR 15-JAN-1999; 99US-0116023.
 XX (GETH) GENENTECH INC.
 XX Presta LG;
 PI WPI; 2000-476035/41.
 XX
 XX New Fc region-containing polypeptides that have altered effector
 PT function due to one or more amino acid modifications in the Fc region,
 PT useful in the treatment of cancer and allergic conditions such as
 PT asthma -
 XX
 XX Disclosure; Fig 4A; 132pp; English.
 XX
 XX The present sequence represents the E27 and anti-IgE antibody light
 CC chain. The protein is used to produce Fc region-containing polypeptides
 CC that have altered effector function as a consequence of one or more
 CC amino acid modifications in the Fc region. The variant polypeptides are
 CC useful for treating cancer, allergic conditions such as asthma (with an
 CC anti-IgE antibody), and LFA-1-mediated disorders. Where the polypeptide
 CC binds the HER2 receptor, the disorder preferably is HER2-expressing
 CC cancer, e.g. a benign or malignant tumour characterized by overexpression
 CC of the HER2 receptor. Such cancers include breast cancer, squamous cell
 CC cancer, small-cell lung cancer, non-small cell lung cancer,
 CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
 CC cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer,
 CC colorectal cancer, endometrial carcinoma, salivary gland carcinoma,
 CC kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid
 CC cancer, hepatic carcinoma and various types of head and neck cancer.
 XX
 SQ Sequence 218 AA;
 Query Match 98.0%; Score 1112; DB 21; Length 218;
 Best Local Similarity 98.2%; Pred. No. 6.2e-56;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSLSASVGDVRVITTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSLSASVGDVRVITTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGTDFLTLTISLQPEDPATYVCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 DB 61 GVPSRFGSGSGTDFLTLTISLQPEDPATYVCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 QY 121 IFPPSDQLKSGTASVVCLLNFPYPRKAYQWKVDNALQSGNSQESVTEQDSKDSYSL 180
 DB 121 IFPPSDQLKSGTASVVCLLNFPYPRKAYQWKVDNALQSGNSQESVTEQDSKDSYSL 180
 QY 181 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
 RESULT 9
 AAB74211
 ID AAB74211 standard; protein; 218 AA.
 XX AAB74211;
 AC AAB74211;
 XX 17-MAY-2001 (first entry)
 XX
 XX E27 anti-IgE antibody light chain.
 DE
 XX Antibody; antigen; cancer; allergy; asthma; LFA-mediated;
 KW autolimmune; vasculitis.
 XX
 OS Unidentified.
 XX
 XX US6194551-B1.
 XX
 XX 27-FEB-2001.
 PD
 XX

PF 31-MAR-1999; 99US-0282505.
 XX
 PR 02-APR-1998; 98US-0080447.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Idusogie EE, Presta LG, Mulkerrin MG;
 XX
 DR WPI; 2001-217935/22.
 XX
 XX Novel polypeptide variant useful for treating cancers, allergic
 PT diseases such as asthma and autoimmune diseases, comprises human
 PT immunoglobulin-G Fc region, retains the ability to bind antigen and
 PT does not activate complement
 XX
 PS Disclosure; Fig 4; 30pp; English.
 XX
 CC The present invention relates to a variant of an antibody
 CC having a human immunoglobulin (Ig)G Fc region, with an
 CC amino acid substitution. The mutant retains the ability to
 CC bind antigen. The invention is useful for determining the
 CC presence of a protein of interest, by exposing the sample
 CC suspected of containing the protein to the antibody and
 CC determining the binding of it to the sample. The antibody
 CC is also useful for treating cancer, allergic conditions
 CC including asthma, LFA-mediated disorders, autoimmune
 CC disorders and vasculitis.
 XX
 SQ Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 22; Length 218;
 Best Local Similarity 98.2%; Pred. No. 6.2e-56;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVITTCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLES 60
 Db 1 DIQLTQSPSSLSASVGRVITTCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLES 60
 Qy 61 GVPFRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 Db 61 GVPFRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 Qy 121 IFPPSDQLKSGTASVYVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 Db 121 IFPPSDQLKSGTASVYVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 Qy 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
 AAW95669
 ID AAW95669 standard; protein; 218 AA.
 XX
 AC AAW95669;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2 fragment.
 XX
 KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria; F(ab)'2 fragment.
 XX
 OS Mus musculus.
 XX
 PN WO9901556-A2.
 XX
 PD 14-JAN-1999.
 XX
 PF 30-JUN-1998; 98WO-US13410.

XX 02-JUL-1997; 97US-0887352.
 PR (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Lowe J, Lowman HB, Presta LG;
 XX
 DR WPI; 1999-106057/09.
 XX
 XX Improving affinity of polypeptides, particularly anti-IgE antibodies
 PT - by identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against
 PT the target
 XX
 PS Disclosure; Page 104; 129pp; English.
 XX
 CC The sequence is that of the variable light chain F(ab)'2 fragment of e26
 CC and e27. It was used as part of a method to improve the affinity of
 CC anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can
 CC be used for reducing or preventing IgE mediated production of
 CC histamine in a mammal. They can be used for treating a disorder
 CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,
 CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic
 CC shock and urticaria. The antibodies can also be used for affinity
 CC purification, detection and diagnosis.
 XX
 SQ Sequence 218 AA;

Query Match 97.7%; Score 1109; DB 20; Length 218;
 Best Local Similarity 97.7%; Pred. No. 9.2e-56;
 Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVITTCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLES 60
 Db 1 DIQLTQSPSSLSASVGRVITTCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLES 60
 Qy 61 GVPFRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 Db 61 GVPFRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 Qy 121 IFPPSDQLKSGTASVYVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 Db 121 IFPPSDQLKSGTASVYVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 Qy 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
 AAW95664
 ID AAW95664 standard; protein; 218 AA.
 XX
 AC AAW95664;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Mus musculus anti-IgE e26 & e27 variable light chain Fab fragment.
 XX
 KW Variable light Fab fragment; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria; IgE.
 XX
 OS Mus musculus.
 XX
 PN WO9901556-A2.
 XX
 PD 14-JAN-1999.
 XX
 PF 30-JUN-1998; 98WO-US13410.
 XX
 PR 02-JUL-1997; 97US-0887352.

XX PA (GETH) GENENTECH INC.

XX PI Jardieu PM, Lowe J, Lowman HB, Presta LG;

XX DR WPI; 1999-106057/09.

XX PT Improving affinity of polypeptides, particularly anti-IgE antibodies

XX PT - by identifying aspartyl residues which undergo isomerisation and

XX PT substituting alternative residues and screening for affinity against

XX PT the target

XX PS Disclosure; Pages 99-100; 129pp; English.

XX CC The sequence is that of the variable light Fab fragment of e26 and e27.

XX CC It was used as part of a method to improve the affinity of anti-IgE

XX CC antibodies such as e26 and e27. The e26 and e27 antibodies can

XX CC be used for reducing or preventing IgE mediated production of

XX CC histamine in a mammal. They can be used for treating a disorder

XX CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,

XX CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic

XX CC shock and urticaria. The antibodies can also be used for affinity

XX CC purification, detection and diagnosis.

XX CC Sequence 218 AA;

SQ Query Match 97.7%; Score 1109; DB 20; Length 218;

Best Local Similarity 97.7%; Pred. No. 9.2e-56;

Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPSRFSGSGSGDFTLTITSSLOPEDFATYICQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Db 61 GVPSRFSGSGSGDFTLTITSSLOPEDFATYICQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYEKHKVACEVTHOGLSSPVTKSFNRGEC 218

Db 181 STLTLSKADYEKHKVACEVTHOGLSSPVTKSFNRGEC 218

RESULT 12

AAB47087

ID AAB47087 standard; protein; 218 AA.

XX AC AAB47087;

XX DT 08-MAY-2001 (first entry)

XX DE Anti-IgE antibody, E26, light chain.

XX KW Light chain; heavy chain; anti-IgE antibody; E26; transfection;

XX KW green fluorescent protein; GFP; promoter; expression.

XX OS Chimeric - Homo sapiens.

XX OS Chimeric - Mus musculus.

XX PN WO200104306-A1.

XX XX 18-JAN-2001.

XX PF 11-JUL-2000; 2000WO-US18841.

XX PR 12-JUL-1999; 99US-0143360.

XX PA (GETH) GENENTECH INC.

PI Chisholm V, Crowley CW, Krummen LA, Meng YG;

XX WPI; 2001-138352/14.

XX PT Novel polynucleotide construct for screening and obtaining cells

XX PT expressing high levels of desired protein, comprises amplifiable

XX PT selectable gene, fluorescent protein gene and sequence encoding desired

XX PT product -

XX PS Disclosure; Fig 13A; 75pp; English.

XX CC The sequences given in AAB47087-88 represent the light and heavy

XX CC chains of the anti-IgE antibody, E26. These sequences were expressed

XX CC by the construct of the invention, which comprises an amplifiable

XX CC selectable gene, a green fluorescent protein gene (GFP), and a

XX CC selected sequence encoding a desired product, which is operably

XX CC linked to either the amplifiable selectable gene or to the GFP gene,

XX CC and to a promoter. Constructs such as this, are useful for producing

XX CC a desired product by introduction into a suitable eukaryotic cell,

XX CC culturing the resultant eukaryotic cell under conditions so as to

XX CC express the desired product, and recovering the desired product from

XX CC the culture medium. The constructs are efficient for identifying and

XX CC selecting for stable eukaryotic cells expressing high levels of a

XX CC desired product. They are suitable for earlier and faster screening

XX CC of transfected cells.

XX CC Sequence 218 AA;

SQ Query Match 97.7%; Score 1109; DB 22; Length 218;

Best Local Similarity 97.7%; Pred. No. 9.2e-56;

Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPSRFSGSGSGDFTLTITSSLOPEDFATYICQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Db 61 GVPSRFSGSGSGDFTLTITSSLOPEDFATYICQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYEKHKVACEVTHOGLSSPVTKSFNRGEC 218

Db 181 STLTLSKADYEKHKVACEVTHOGLSSPVTKSFNRGEC 218

RESULT 13

AAB76949

ID AAB76949 standard; Protein; 218 AA.

XX AC AAB76949;

XX DT 17-APR-2001 (first entry)

XX DE Full length light chain sequence of e26 SEQ ID 15.

XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;

XX KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;

XX KW conjunctivitis; eczema; urticaria; food allergy.

XX OS Synthetic.

XX PN US6172213-B1.

XX PD 09-JAN-2001.

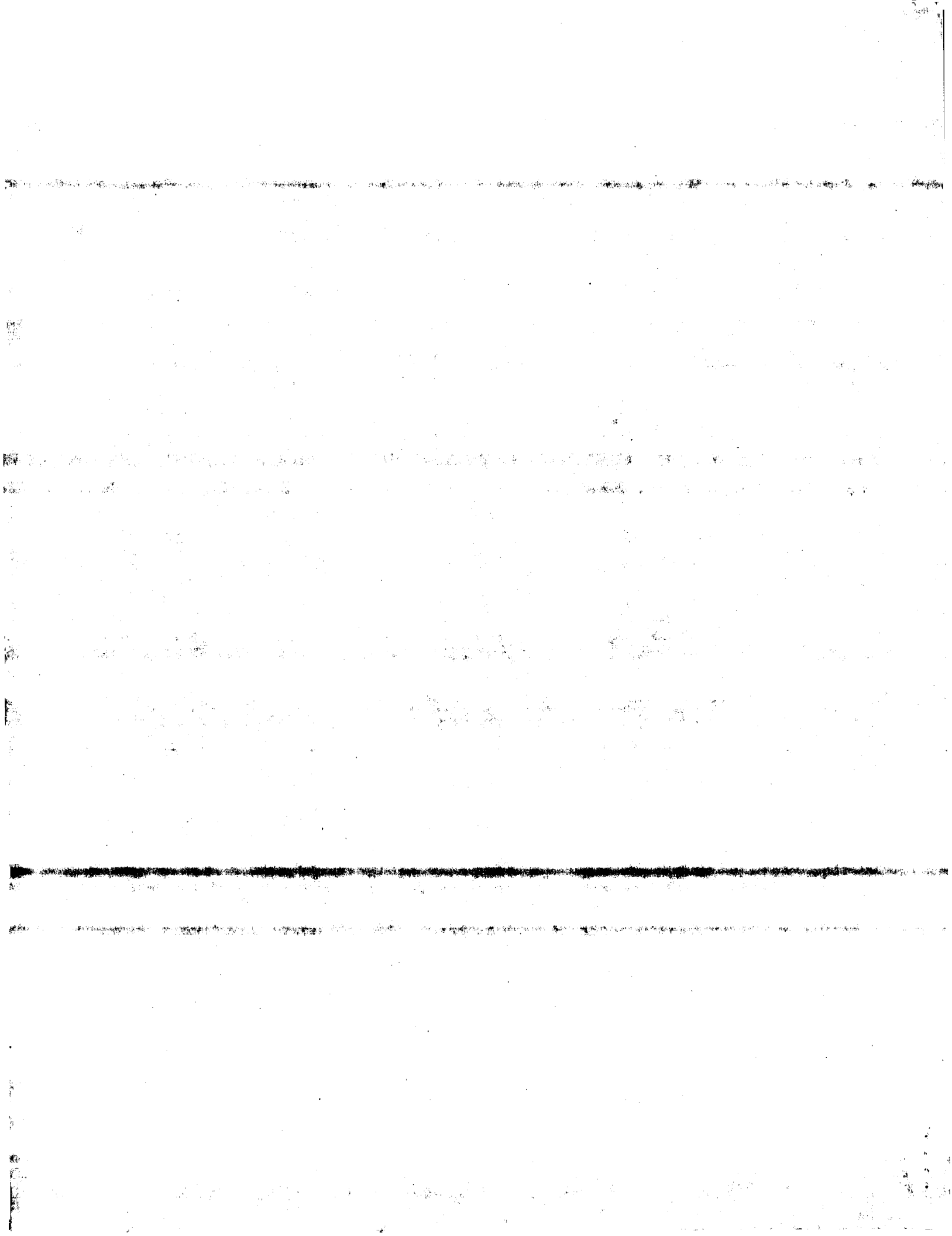
XX PF 30-JUN-1998; 98US-0109207.

XX PR 02-JUL-1997; 97US-0051554.

KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
OS Synthetic.
XX
XX US6172213-B1.
PN
XX
XX 09-JAN-2001.
PD
XX
XX 30-JUN-1998; 98US-0109207.
PF
XX
XX 02-JUL-1997; 97US-0051554.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
PI
XX
XX WPI; 2001-122353/13.
DR
XX
XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display
XX
PS Claim 1; Fig 13; 87pp; English.
XX
XX This invention relates to a nucleotide sequence encoding an antibody
CC with improved anti-IgE antibody activity. The antibody has improved
CC action due to a process comprising, a) identifying aspartyl residues
CC prone to isomerization in unimproved anti-IgE (immunoglobulin E)
CC antibody; b) substituting alternative residues to create candidate
CC molecules, and c) selecting those candidate molecules which display
CC affinity against the target molecule. Use of the antibody results in
CC antiasthmatic; antiallergic; ophthalmological; dermatological and
CC antiinflammatory activity. The antibodies are useful for treating
CC IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
CC eczema, urticaria and food allergies. The mutant antibodies produced by
CC the above mentioned nucleic acids may also be used as affinity
CC purification agents and in diagnostic assays for detecting the expression
CC of an antigen of interest in specific cell, tissues or serum. Amino acid
CC sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of
CC the invention. Polynucleotide sequence AAF69253 represents an expression
CC plasmid used in the course of the invention, and oligonucleotides
CC AAF69254 - AAF69271 are used in the generation of affinity improved
CC anti-IgE antibodies.
XX
SQ Sequence 218 AA;

Query Match 97.7%; Score 1109; DB 22; Length 218;
Best Local Similarity 97.7%; Pred. No. 9.2e-56;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMNWYQOKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSPRFGSGSGTDFLTITSSLPQDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
DB 61 GVPSPRFGSGSGTDFLTITSSLPQDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218



QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 2

US-08-466-151-9
; Sequence 9, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-9

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.le-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPS 120

Db 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPS 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 3

US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123P1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAEL1
US-09-109-207C-13

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.le-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPS 120
Db 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPS 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 4

US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1P
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:

```
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAEL1
US-09-296-005-13

Query Match      100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||
Db 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||

QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||
Db 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||

QY 121 IPPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||||
Db 121 IPPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||||

QY 181 STLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 218
   |||||
Db 181 STLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 218
   |||||
```

```
RESULT 5
US-08-466-163B-9
; Sequence 9, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael1, version 1, light chain
US-08-466-163B-9
```

```
Query Match      100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||
Db 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||

QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||
Db 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||

QY 121 IPPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||||
Db 121 IPPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||||

QY 181 STLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 218
   |||||
Db 181 STLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 218
   |||||
```

RESULT 6

```
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1
```

```
Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||
Db 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||

QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||
Db 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||

QY 121 IPPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||||
Db 121 IPPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||||

QY 181 STLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 218
   |||||
Db 181 STLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 218
   |||||
```

RESULT 7

```
US-09-054-255-1
; Sequence 1, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1
```

```
Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||
Db 1 DIQLTQSPSLSASVGDRTVITCRASQSDVDYDGSYNNWYQOKPGKAPKLLIIAASVLES 60
   |||||

QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYTCQSHEDPYTFQGGTKVEIKRTVAAPSVF 120
   |||||
```

Db 61 GVPSPSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IFPPDEQLKSGTASVVCLLNPNYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPDEQLKSGTASVVCLLNPNYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8

US-09-282-846-1
; Sequence 1, Application US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/09/282.846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-1

Query Match 98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
Db 61 GVPSPSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IFPPDEQLKSGTASVVCLLNPNYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPDEQLKSGTASVVCLLNPNYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9

US-09-680-145-1
; Sequence 1, Application US/09680145
; Patent No. 6538124
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/680,145
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/282,505
; PRIOR FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6538124
US-09-680-145-1
Query Match 98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
Db 61 GVPSPSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IFPPDEQLKSGTASVVCLLNPNYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPDEQLKSGTASVVCLLNPNYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10

US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60


```
Qy 61 GVPFRFSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Qy 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFRNREC 218
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFRNREC 218

RESULT 11
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887.352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Qy 61 GVPFRFSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Qy 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFRNREC 218
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFRNREC 218

RESULT 12
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887.352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Qy 61 GVPFRFSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Qy 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFRNREC 218
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFRNREC 218

RESULT 13
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-24

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQOKPGKAPKLLIYAASYLE 60
Qy 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYVCOQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYVCOQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 14
US-09-109-207C-15
Sequence 15, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 15
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-218
OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15

Query Match 97.7%; Score 1109; DB 3; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;

Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQOKPGKAPKLLIYAASYLE 60
Qy 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYVCOQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYVCOQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 15
US-09-109-207C-17
Sequence 17, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 17
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-218
OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17

Query Match 97.7%; Score 1109; DB 3; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQOKPGKAPKLLIYAASYLE 60
Qy 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYVCOQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYVCOQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

Search completed: August 12, 2003, 16:32:55
Job time : 10.4218 secs

| | | | | | |
|----|-----|---------------------|-------------------------|-----------------------|-----|
| Qy | 61 | GVPSRFSGSGGTFTLT | ISSLPQEDFATYYCQSHEDPYT | FGQGTKEVKEIKRTVAAPSVF | 120 |
| | | | | | |
| Db | 61 | GVPSRFSGSGGTFTLT | ISSLPQEDFATYYCQSHEDPYT | FGQGTKEVKEIKRTVAAPSVF | 120 |
| | | | | | |
| Qy | 121 | IFPPDEQLKGTASVWCLLN | FNYPRAKVGQVDNALQSGNSQES | VTQDSKDSITYSL | 180 |
| | | | | | |
| Db | 121 | IFPPDEQLKGTASVWCLLN | FNYPRAKVGQVDNALQSGNSQES | VTQDSKDSITYSL | 180 |
| | | | | | |
| Qy | 181 | STLTLSKADYEKKHYACEV | THQGLSPVTKSFNRGEC | 218 | |
| | | | | | |
| Db | 181 | STLTLSKADYEKKHYACEV | THQGLSPVTKSFNRGEC | 218 | |
| | | | | | |

RESULT 2
US-09-802-096--9
; Sequence 9, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C30US
; CURRENT APPLICATION NUMBER: US/09/802.096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1, light chain
US-09-802-096--9

RESULT 3
US-09-920-171-13
; Sequence 13, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John

```

; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-13

Query Match 100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 218; Conservative 0; Mismatches 0; Indels 0

Qy 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGDSDYNNWYQQKPGKAPKLLI
Db 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGDSDYNNWYQQKPGKAPKLLI
Qy 61 GVPSPFSGSGSTDEFTLTLTSSIQPEDFATVYCCQSHEDPYTFGGGTGKVEIKR
Db 61 GVPSPFSGSGSTDEFTLTLTSSIQPEDFATVYCCQSHEDPYTFGGGTGKVEIKR
Qy 121 IFPPSDEQLKSGTASVCLLNINFPYPREAKVQWKVDNALQSGNSQESVTEQDS
Db 121 IFPPSDEQLKSGTASVCLLNINFPYPREAKVQWKVDNALQSGNSQESVTEQDS
Qy 181 STLTLSKADYEKKHYVACEVTHQGLSSPVTKSNRGC 218
Db 181 STLTLSKADYEKKHYVACEVTHQGLSSPVTKSNRGC 218

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```

RESULT 4
US-09-925-179-9
; Sequence 9, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1, light chain
US-09-925-179-9

```

QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLLNNEYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVCLLNNEYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-09-925-179-67
; Sequence 67, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1CIUS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 67
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length light chain sequence corresponding to F(ab)9 of Table
US-09-925-179-67

Query Match 98.7%; Score 1120; DB 11; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.9e-72;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLLNNEYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVCLLNNEYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-09-920-171-15

; Sequence 15, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-15

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.2e-71;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGSYMNWYQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLLNNEYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVCLLNNEYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7

US-09-920-171-17
; Sequence 17, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-17

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.2e-71;

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-917-410-2

Query Match 97.6%; Score 1108; DB 9; Length 218;
Best Local Similarity 97.2%; Pred. No. 1.4e-71;
Matches 212; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTTITCRASQSDVDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQMTQSPSSLSASVGRVTTITCKASQSDVDYDGDSDYNNWYQOKPGKAPKLLIYAASNLE 60

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GIPFRFSGSGGTDFTLTITSLQPEDFATYYCQSNEDPRTFGGTVKVEIKRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180

Qy 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
US-10-216-484-127
Sequence 127, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 127
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-127

Query Match 96.9%; Score 1100; DB 15; Length 238;
Best Local Similarity 97.7%; Pred. No. 5.5e-71;
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTTITCRASQSDVDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
Db 21 DIVLTQSPSSLSASVGRVTTITCKASQSDVDYDGDSDYNNWYQOKPGKAPKLLIYAASNLE 80

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 81 GVPFRFSGSGGTDFTLTITSLQPEDFATYYCQSNEDPRTFGGTVKVEIKRTVAAPSVF 140

Qy 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 141 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200

Qy 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 201 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 12
US-10-216-484-131
Sequence 131, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-131

Query Match 96.8%; Score 1099; DB 15; Length 238;
Best Local Similarity 97.2%; Pred. No. 6.5e-71;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVTTITCRASQSDVDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
Db 21 DIVLTQSPSSLSASVGRVTTITCKASQSDVDYDGDSDYNNWYQOKPGKAPKLLIYAASNLE 80

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 81 GIPFRFSGSGGTDFTLTITSLQPEDFATYYCQSNEDPRTFGGTVKVEIKRTVAAPSVF 140

Qy 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 141 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200

Qy 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 201 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 13
US-10-216-484-129
Sequence 129, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:26:07 ; Search time 9.74665 Seconds
(without alignments)
2150.973 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGRVT.....EVTHQGLSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 942.5 | 83.0 | 215 | 2 JE0242 | Ig kappa chain NIG |
| 2 | 917.5 | 80.8 | 215 | 2 JE0244 | Ig kappa chain NIG |
| 3 | 892.5 | 78.6 | 215 | 2 JE0243 | Ig kappa chain NIG |
| 4 | 883 | 77.8 | 216 | 2 JE0241 | Ig kappa chain Am3 |
| 5 | 875.5 | 77.1 | 215 | 2 A23746 | Ig kappa chain V-I |
| 6 | 759 | 66.9 | 240 | 2 S06084 | Ig kappa chain pre |
| 7 | 739 | 65.1 | 218 | 2 S68241 | Ig kappa chain v r |
| 8 | 737 | 64.9 | 218 | 2 JC5810 | Ig kappa chain v r |
| 9 | 727 | 64.1 | 230 | 2 S33161 | monoclonal antibod |
| 10 | 723 | 63.7 | 220 | 2 A31790 | Ig kappa chain - s |
| 11 | 718 | 63.3 | 234 | 2 S14237 | Ig kappa chain v r |
| 12 | 716 | 63.1 | 234 | 2 S01320 | Ig kappa chain pre |
| 13 | 712 | 62.7 | 210 | 2 A56169 | Ig kappa chain v r |
| 14 | 699 | 61.6 | 214 | 2 S68212 | Ig kappa chain (Ma |
| 15 | 698.5 | 61.5 | 219 | 2 S38865 | Ig kappa chain - m |
| 16 | 694.5 | 61.2 | 217 | 2 S42772 | Ig kappa chain - m |
| 17 | 693.5 | 61.1 | 225 | 2 S37484 | Ig kappa chain - m |
| 18 | 692.5 | 61.0 | 219 | 2 PC4203 | Ig kappa chain (mo |
| 19 | 689.5 | 60.7 | 219 | 2 S52028 | Ig kappa chain - m |
| 20 | 687.5 | 60.6 | 235 | 2 S25058 | Ig kappa chain - m |
| 21 | 683.5 | 60.2 | 219 | 2 S16112 | Ig kappa chain v r |
| 22 | 670.5 | 59.1 | 225 | 2 JL0029 | Ig kappa chain pre |
| 23 | 608 | 53.6 | 135 | 2 S52059 | JC-kappa chain pre |
| 24 | 596 | 52.5 | 178 | 2 PT0219 | Ig kappa chain v-C |
| 25 | 563.5 | 49.6 | 229 | 2 A20969 | Ig kappa chain pre |
| 26 | 548 | 48.3 | 106 | 1 K3HU | Ig kappa chain C r |
| 27 | 535.5 | 47.2 | 197 | 2 S29593 | Ig kappa chain (WM |
| 28 | 534.5 | 47.1 | 238 | 2 A49633 | Ig lambda-like cha |
| 29 | 513 | 45.2 | 99 | 2 A37927 | Ig kappa chain C r |

ALIGNMENTS

RESULT 1

JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappatype light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 942.5; DB 2; Length 215;
Best Local Similarity 83.5%; Pred. No. 1.3e-55;
Matches 182; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQKRGKAPKLLIYAASYLE 60
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSV---SNNYLAWYQKPGQAPSLIYDASSRAT 57
QY 61 GVPRESGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
Db 58 GIPDRFSGSGSGTDFLTITSLGLEPDAFYVYCOYDRPPMTFGQTKVEIKRTVAAPSVF 117
QY 121 IFPPSDEQLKSGTASVIVCLINNEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 118 IFPPSDEQLKSGTASVIVCLINNEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 177
QY 181 STLTSLKADYKHKYACEVTHQGLSPVTKSFNRGEC 218
Db 178 STLTSLKADYKHKYACEVTHQGLSPVTKSFNRGEC 215

RESULT 2

JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 883; DB 2; Length 216;
Best Local Similarity 79.4%; Pred. No. 11e-51;
Matches 173; Conservative 17; Mismatches 26; Indels 2; Gaps 2;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
DB 1 EVLVTQSPATLSVSPGERATLSCRASQSV---HSLAWYQKPKQAPRLIYRSTRAT 56
QY 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGGTKEIKRTVAAPSV 119
DB 57 GIPARFSGSGSGTDFLTITSSLOSEDFALYYCOQNTWPTLFTGGGTKEIKRTVAAPSV 116
QY 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 179
DB 117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 176
QY 180 STLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 218
DB 177 SSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 215

RESULT 3
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amyloidosis
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 892.5; DB 2; Length 215;
Best Local Similarity 81.3%; Pred. No. 2.7e-52;
Matches 176; Conservative 16; Mismatches 20; Indels 5; Gaps 2;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSV---ATNVVMTQKLGQAPRLIYDASTRAT 56
QY 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGGTKEIKRTVAAPSV 119
DB 57 GVPARFSGSGSGTDFLTITSSLOSEDFALYYCOHNNAPPTFGGTKEIKRTVAAPSV 116
QY 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 179
DB 117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 176
QY 180 SSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 218
DB 177 SSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 215

RESULT 4
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu chain c
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 875.5; DB 2; Length 215;
Best Local Similarity 81.1%; Pred. No. 3.5e-51;
Matches 176; Conservative 13; Mismatches 25; Indels 3; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
DB 1 EIVLTQSPATLSVSPGERATLSCRASQSV---SSNYLAWYQKPKQAPRLIYDASSRAT 57
QY 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGGTKEIKRTVAAPSV 120
DB 58 GIPDRFSGSGSGTDFLTITSSLOPEDFATYYCOQYQYSSPLTFGGGTKEIKRTVAAPSV 117
QY 121 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 180
DB 118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 177
QY 181 STLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGE 217
DB 178 STLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGE 214

RESULT 5
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 875.5; DB 2; Length 215;
Best Local Similarity 81.1%; Pred. No. 3.5e-51;
Matches 176; Conservative 13; Mismatches 25; Indels 3; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
DB 1 EIVLTQSPATLSVSPGERATLSCRASQSV---SSNYLAWYQKPKQAPRLIYDASSRAT 57
QY 61 GVPFRFSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGGTKEIKRTVAAPSV 120
DB 58 GIPDRFSGSGSGTDFLTITSSLOPEDFATYYCOQYQYSSPLTFGGGTKEIKRTVAAPSV 117
QY 121 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 180
DB 118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 177
QY 181 STLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGE 217
DB 178 STLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGE 214

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3, rat myeloma immunoglobulin kappa chain c
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084

[illegible]

Query Match 62.7%; Score 712; DB 2; Length 210;
Best Local Similarity 64.6%; Pred. No. 2.2e-40;
Matches 135; Conservative 28; Mismatches 46; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIVLTQSPASLTATSLQGRATISCRASKSVSSGYSYNNHWYQKPGQPKVLIYASL 60
QY 61 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGTKVEIKRTVAAPSV 120
DB 61 GVPFRSGSGSGTDFLTINHPVEEDAATYYCQHSRELPTWFGGKLEIKRADAAPTV 120
QY 121 IFPPSDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 121 IFPPSDEQLTSGGASVVCVCLNNFYPKDINVKWKIDGSRQNGVLNSWTQDSKDSYMS 180
QY 181 STLTLSKADYEKKHYKVIACEVTHOGLSSPV 209
DB 181 STLTLTDEYERHNSYTCETHKTSTSPI 209

RESULT 14
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 61.6%; Score 699; DB 2; Length 214;
Best Local Similarity 61.7%; Pred. No. 1.6e-39;
Matches 132; Conservative 34; Mismatches 46; Indels 2; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASYL 58
DB 1 DIVLTQSPSSLSASVGVKVTMSCKSSQSLNSRNQKNYLAQYQKPGQSPKLLIYFASTR 60
QY 59 ESGVPSRFSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGTKVEIKRTVAAPS 118
DB 61 ESGVPSRFSGSGSGTDFLTITSTVQAEADLADYFCQGHYSTPTTFGGGKLEIKRADAAPT 120
QY 119 VFIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 178
DB 121 VSIFPPSDEQLTSGGASVVCVCLNNFYPKDINVKWKIDGSRQNGVLNSWTQDSKDSYSL 180
QY 179 LSSTLTLSKADYEKKHYKVIACEVTHOGLSSPVTKS 212
DB 181 MSSTLTLTDEYERHNSYTCETHKTSTSPIVKS 214

RESULT 15
S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:Z27396; NID:q416538; PIDN:CAA81787.1; PID:q416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.5%; Score 698.5; DB 2; Length 219;
Best Local Similarity 60.3%; Pred. No. 1.8e-39;
Matches 132; Conservative 34; Mismatches 52; Indels 1; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASYLE 59
DB 1 ELVMTQSPLSVLSVGLDQASISCRSSQSLVHTNGTYLHWYLOKPGLSPLLIYIVSNRF 60
QY 60 SGVPSRFSGSGSGTDFLTITSSLOPEDFATYYCOQSHEDPYTFGGTKVEIKRTVAAPSV 119
DB 61 SGVPSRFSGSGSGTDFLTIKISRVEADLGVYFCQVTHVPWTFGGGKLEIKRADAAPTV 120
QY 120 FIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
DB 121 SIFPPSDEQLTSGGASVVCVCLNNFYPKDINVKWKIDGSRQNGVLNSWTQDSKDSYSL 180
QY 180 SSTLTLSKADYEKKHYKVIACEVTHOGLSSPVTKSFNRGEC 218
DB 181 SSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNREGC 219

Search completed: August 12, 2003, 16:32:19
Job time : 10.7466 secs

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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:22:22 ; Search time 5.84799 seconds
(without alignments)
1753.051 Million cell updates/sec

Title: US-09-802-077-9

Perfect score: 1135

Sequence: 1 DIQLQSPSSLASVGDRT.....EVTHQGLSPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|------------|---------------------|
| 1 | 548 | 48.3 | 106 | KAC_HUMAN | P01834 homo sapien |
| 2 | 471 | 41.5 | 108 | KV1H_HUMAN | P01600 homo sapien |
| 3 | 467 | 41.1 | 111 | KV3M_MOUSE | P01665 mus musculus |
| 4 | 463 | 40.8 | 108 | KV1E_HUMAN | P01597 homo sapien |
| 5 | 462 | 40.7 | 111 | KV3Q_MOUSE | P01667 mus musculus |
| 6 | 460 | 40.5 | 111 | KV3N_MOUSE | P01666 mus musculus |
| 7 | 460 | 40.5 | 129 | KV1W_HUMAN | P04431 homo sapien |
| 8 | 459 | 40.4 | 111 | KV3Q_MOUSE | P01669 mus musculus |
| 9 | 455 | 40.4 | 111 | KV3L_MOUSE | P01664 mus musculus |
| 10 | 454 | 40.0 | 108 | KV1V_HUMAN | P04430 homo sapien |
| 11 | 452 | 39.8 | 108 | KV1V_HUMAN | P01606 homo sapien |
| 12 | 448 | 39.5 | 108 | KV1B_HUMAN | P01594 homo sapien |
| 13 | 448 | 39.5 | 108 | KV1M_HUMAN | P01605 homo sapien |
| 14 | 446.5 | 39.3 | 110 | KV3P_MOUSE | P01668 mus musculus |
| 15 | 444 | 39.1 | 108 | KV1K_HUMAN | P01603 homo sapien |
| 16 | 444 | 39.1 | 108 | KV1S_HUMAN | P01611 homo sapien |
| 17 | 443 | 39.0 | 108 | KV1F_HUMAN | P01598 homo sapien |
| 18 | 443 | 39.0 | 108 | KV1Q_HUMAN | P01607 homo sapien |
| 19 | 442 | 38.9 | 108 | KV1G_HUMAN | P01599 homo sapien |
| 20 | 441 | 38.9 | 108 | KV1Y_HUMAN | P80362 homo sapien |
| 21 | 439 | 38.7 | 108 | KV1P_HUMAN | P01610 homo sapien |
| 22 | 438 | 38.6 | 108 | KV1P_HUMAN | P01608 homo sapien |
| 23 | 437 | 38.5 | 108 | KV1L_HUMAN | P01604 homo sapien |
| 24 | 431 | 38.0 | 108 | KV1A_HUMAN | P01593 homo sapien |
| 25 | 430.5 | 37.9 | 109 | KV1T_HUMAN | P01612 homo sapien |
| 26 | 429.5 | 37.8 | 107 | KV1D_HUMAN | P01596 homo sapien |
| 27 | 429 | 37.8 | 111 | KV3H_MOUSE | P01660 mus musculus |
| 28 | 425 | 37.4 | 108 | KV1Q_HUMAN | P01609 homo sapien |
| 29 | 423 | 37.3 | 108 | KV1C_HUMAN | P01595 homo sapien |
| 30 | 420 | 37.0 | 111 | KV3J_MOUSE | P01662 mus musculus |
| 31 | 419 | 36.9 | 129 | KV1X_HUMAN | P04432 homo sapien |
| 32 | 415 | 36.6 | 131 | KV3I_MOUSE | P01661 mus musculus |
| 33 | 411 | 36.2 | 111 | KV3K_MOUSE | P01663 mus musculus |

ALIGNMENTS

RESULT 1

| ID | KAC_HUMAN | STANDARD; | PRT; | 106 AA. |
|----|---|-----------|------|---------|
| AC | P01834; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ig kappa chain C region. | | | |
| GN | IGKC. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE (MYELOMA PROTEIN EU). | | | |
| RX | MEDLINE=71064023; PubMed=5489770; | | | |
| RA | Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."; | | | |
| RT | RT Biochemistry 9:3155-3161(1970). | | | |
| RN | [2] | | | |
| RP | DISULFIDE BONDS. | | | |
| RX | MEDLINE=71064027; PubMed=4923144; | | | |
| RA | Gall W.E., Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."; | | | |
| RT | Biochemistry 9:3188-3196(1970). | | | |
| RN | [3] | | | |
| RP | SEQUENCE (BENCE-JONES PROTEIN TI). | | | |
| RX | MEDLINE=72188439; PubMed=5027703; | | | |
| RA | Suter L., Barnikol H.U., Watanabe S., Hilschmann N.; | | | |
| RT | "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."; | | | |
| RT | Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=81042304; PubMed=6775818; | | | |
| RA | Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.; | | | |
| RT | "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."; | | | |
| RT | Cell 22:197-207(1980). | | | |
| RN | [5] | | | |
| RP | SEQUENCE (BENCE-JONES PROTEIN ROY). | | | |
| RA | Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.; | | | |
| RT | (in) Franek F., Shugar D. (eds.); | | | |
| RT | Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969). | | | |
| RN | [6] | | | |
| RP | SEQUENCE (BENCE-JONES PROTEIN CUM). | | | |
| RX | MEDLINE=68242259; PubMed=5586923; | | | |
| RA | Hilschmann N.; | | | |
| RT | "The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."; | | | |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 410 | 36.1 | 114 | 1 | KV4A_HUMAN | P01625 homo sapien |
| 35 | 410 | 36.1 | 134 | 1 | KV4C_HUMAN | P06314 homo sapien |
| 36 | 404 | 35.6 | 111 | 1 | KV3R_MOUSE | P01670 mus musculus |
| 37 | 404 | 35.6 | 111 | 1 | KV3S_MOUSE | P01671 mus musculus |
| 38 | 404 | 35.6 | 112 | 1 | KV1U_HUMAN | P01613 homo sapien |
| 39 | 404 | 35.6 | 112 | 1 | KV3G_MOUSE | P01659 mus musculus |
| 40 | 404 | 35.6 | 132 | 1 | KV3F_MOUSE | P01658 mus musculus |
| 41 | 402 | 35.4 | 117 | 1 | KV1J_HUMAN | P01602 homo sapien |
| 42 | 400.5 | 35.3 | 129 | 1 | KV3L_HUMAN | P18135 homo sapien |
| 43 | 399.5 | 35.2 | 129 | 1 | KV3M_HUMAN | P18136 homo sapien |
| 44 | 399 | 35.2 | 111 | 1 | KV3U_MOUSE | P01673 mus musculus |
| 45 | 396.5 | 34.9 | 109 | 1 | KV3B_HUMAN | P01620 homo sapien |

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
RN [9]
RP SEQUENCE OF 1-33; 38-41 AND 62-80.
RC TISSUE=Abdominal adipose tissue;
RX PubMed=9588180;
RA Olsen K.E., Sletten K., Westermark P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00241; AA58989.1; -;
DR EMBL; V00557; CAA23823.1; -;
DR PIR; B90562; K3HU.
DR PDB; 1D5B; 09-FEB-00.
DR PDB; 1D5I; 09-FEB-00.
DR PDB; 1D6V; 04-OCT-00.
DR PDB; 1HEZ; 10-AUG-01.
DR PDB; 1HLK; 12-MAR-97.
DR PDB; 1I72; 08-AUG-01.
DR PDB; 1IMW; 15-MAY-97.
DR Genew; HGNC:5716; IGKC.
DR MIM; 147200; -;
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT DOMAIN 1 1 IG-LIKE.
FT NON_TER 5 102
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT VARIANT 83 83 /FTID-VAR.003897.
FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 48.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.9e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TVAAPSVFPPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDS 172

Db 1 TVAAPSVFPPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 173 KDSTYSLSSTLTLSKADYKHKVYACVTHOGLSSPVTKSFNRGEC 218
Db 61 KDSTYSLSSTLTLSKADYKHKVYACVTHOGLSSPVTKSFNRGEC 106

RESULT 2
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1H0HU.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 41.5%; Score 471; DB 1; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.5e-32;
Matches 92; Conservative 10; Mismatches 6; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSI-----SSYLSWYQKPKAPVLIYAASLPS 56
QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYQCQSHEDPYTFGQGTVEIKR 112
Db 57 GVPFRFSGSGSGTDFTLTISSLPQEDFATYQCQNYITPTSFQGTVEIKR 108

RESULT 3
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR HSSP; P80362; IWTLL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 41.1%; Score 467; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 3 3e-32;
Matches 86; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGDRTVITCRASQSDYDGDSDYNNYQKPGKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNYQKPGKAPKLLIYAASNL 60

QY 61 GVPSPFSGSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIK 111
Db 61 GIPARFSGSGSGTDFLTINHPVEEDATYCCQSHEDPYTFQGTKEIK 111

RESULT 4
KVLE_HUMAN STANDARD; PRT; 108 AA.
ID KVLE_HUMAN
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01865; KIHUDE.
DR HSSP; P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 40.8%; Score 463; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 6 8e-32;
Matches 89; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQLTQSPSLASVGDRTVITCRASQSDYDGDSDYNNYQKPGKAPKLLIYAASYLE 60
Db 1 BIZMTQSPSLASVGDRTVITCRAGQSV----NKYLNWYQKPGKAPKLVIFAASLSKS 56

QY 61 GVPSPFSGSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKR 112
Db 57 GVPSPFSGSGSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGPGTKVEMTR 108

RESULT 5
KV3O_MOUSE STANDARD; PRT; 111 AA.
ID KV3O_MOUSE
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSSP; P80362; IWTLL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 40.7%; Score 462; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 8 5e-32;
Matches 85; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGDRTVITCRASQSDYDGDSDYNNYQKPGKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNYQKPGKAPKLLIYAASNL 60

Wed Aug 13 09:14:52 2003

us-09-802-077-9.rsp

```
QY 61 GVPFRFSGSGTDTFTLTSSLPEDFATYYCQSHEDPYTFGQTKVEIK 111
DB 61 GIPARFSGSGTDTFTLNIHPVEEDATYYCQSNEDPWTFGSKLEIK 111

RESULT 6
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL Nature 276:785-790(1978).
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 40.5%; Score 460; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 1.2e-31;
Matches 85; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDGDSYMNWYQKPGKAPKLLIYAASLYS 60
DB 1 DIVLTQSPASLVSLGQRAISCKASQSDVDGDSYMNWYQKPGQPPKLLIYAASNL 60

QY 61 GVPFRFSGSGTDTFTLTSSLPEDFATYYCQSHEDPYTFGQTKVEIK 111
DB 61 GIPARFSGSGTDTFTLNIHPVEEDATYYCQSNEDPLTFGAGTKLEIK 111

RESULT 7
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;

RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUWK.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 40.5%; Score 460; DB 1; Length 129;
Best Local Similarity 82.0%; Pred. No. 1.5e-31;
Matches 91; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDGDSYMNWYQKPGKAPKLLIYAASLYS 60
DB 23 DIQMTQSPSSLSASVGDRTTTCRASQSI-----SNLWYQKPGKAPKLLIYAASLSQS 78

QY 61 GVPFRFSGSGTDTFTLTSSLPEDFATYYCQSHEDPYTFGQTKVEIK 111
DB 79 GVTFRFSGSGTDTFTLTSSLPEDSATYYCQSYSTLTITFGQTRLEIK 129

RESULT 8
KV3Q_MOUSE STANDARD; PRT; 111 AA.
ID KV3Q_MOUSE
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL Nature 276:785-790(1978).
DR HSP; P01637; KVM569.
DR PIR; E01937; KVM569.
DR HSP; P80362; 1WTL.
```

Matches 84; Conservative 14; Mismatches 13; Indels 0; Gaps 0

QY 1 DIQLTQSPSSLSASVGRVITTCRASQSDVDYDGSYNNWYQOKPKGKAPKLLIYAASYLES 60
 Db 1 DIVLTQSPASLAVSLGQARITSCASKASQSDYTGESYNNWYQONFGQSPKLLIYAASNLES 60

QY 61 GVPFSRFGSGSGTDFTLTITSSLPEDFATYYCQOSHEDPYTFGGTKVEIKR 111
 Db 61 GIPARFSGSGSGTDFTLTNIHPVEEDAATYYCQOSNEDPYTFGGTKLEIK 111

RESULT 10
 KVIIV_HUMAN STANDARD; PRT; 108 AA.
 ID AC P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region BAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86174817; PubMed=3083240;
 RA Dwulet F.E., O'Connor T.P., Benson M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 RL Mol. Immunol. 23:73-78(1986).
 DR PIR; A01878; KIHUBN.
 DR HSP; P80362; IWLTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Anyloid.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; CD3FD944FE96FD37 CRC64;
 Query Match 40.08; Score 454; DB 1; Length 108;
 Best Local Similarity 81.2; Pred. No. 3.8e-31;
 Matches 91; Conservative 7; Mismatches 10; Indels 4; Gaps 1

QY 1 DIQLTQSPSSLSASVGRVITTCRASQSDVDYDGSYNNWYQOKPKGKAPKLLIYAASYLES 60
 Db 1 DIQLTQSPSSLSASVGRVITTCRASQSDY----YNNVAFQOKPKGKAPKSLYDASTLOS 56

QY 61 GVPFSRFGSGSGTDFTLTITSSLPEDFATYYCQOSHEDPYTFGGTKVEIKR 112
 Db 57 GVPFSNFGSGSGTDFTLTITSSLPEDFATYYCQYNSPYTFGGTKVQIKR 108

RESULT 11
 KVIIN_HUMAN STANDARD; PRT; 108 AA.
 ID AC P01606;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region OU.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE..
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003006; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 39.8%; Score 452; DB 1; Length 108;
Best Local Similarity 70.5%; Pred. No. 5.6e-31;
Matches 79; Conservative 21; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVITTCRASQSDYDGDSTWNNYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTZSPSSLSASVGRVITTCRASZTI-----SSYLWYZZKPGKAPKLLIYAASBLHS 56

QY 61 GVPSRFSGSGGDTFTLTITSSLPEDFATYCCQSHEDPVTFGQTKVEIKR 112
Db 57 GVPSRFSGSGGHTFTTSSLPZBFAFYCCZSYSSPTTFGZGTFLZIKR 108

RESULT 12
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;

RA Fehhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY.
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A91653; KIHUOU.
DR PDB; 1JVS; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig-MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 39.5%; Score 448; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 1.2e-30;
Matches 89; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVITTCRASQSDYDGDSTWNNYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTZSPSSLSASVGRVITTCRASQDI-----SDYLNWYQKPGKAPKLLIYASNLES 56

QY 61 GVPSRFSGSGGDTFTLTITSSLPEDFATYCCQSHEDPVTFGQTKVEIKR 112
Db 57 GVPSRFSGSGGSAHTFTTSSLPEDFATYCCQYDYLPTWTFGQTKVEIKR 108

RESULT 13
KV1M_HUMAN
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHUOL.
DR HSSP; P01607; 1REI.

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 39.5%; Score 448; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 1.2e-30;
Matches 88; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIQMTQSPSSLSVSGDRVTTCASQNV---NAYLNWYQKPGKAPKLLIYGASTREA 56

Qy 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKR 112
Db 57 GVPFRFSGSGGTDFTLTISLQPEDIATYYCQYNNWPTFGGTKVEIKR 108

RESULT 14
KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;
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Query Match 39.3%; Score 446.5; DB 1; Length 110;
Best Local Similarity 75.7%; Pred. No. 1.6e-30;
Matches 84; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIVLTQSPASLAVSLGQRATISCASQSLDVGSDYNNWYQKPGQPPKLLIYAASNL 60

Qy 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKR 111
Db 61 GIPARFSGSGGTDFTLTNIHPVEEEDAAATYYCHQS-EDPWFSGTKLEIKR 110

RESULT 15
KV1K_HUMAN STANDARD; PRT; 108 AA.
ID KV1K_HUMAN
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 39.1%; Score 444; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 2.6e-30;
Matches 84; Conservative 14; Mismatches 10; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIQMTQSPSTLSVSGDRVTTCASQIV---LSYLNWYQKPGKAPKLLIYAASSLET 56

Qy 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKR 112
Db 57 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQYNNWPTFGGTKVDLKR 108

Search completed: August 12, 2003, 16:30:28
Job time : 5.84799 secs
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Db      77  GVPAFFSGSGSTFTLTIISSQSEDFAVIYCOQNKWPHTEGQGTAKDKIKRTVAAPSVF 136
      121  IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
      137  IFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 196
      181  STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
      197  STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 2
Q8NEK0
ID      Q8NEK0      PRELIMINARY;      PRT;      239 AA.
AC      Q8NEK0;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Prostate;
RA      Strausberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC030814; AAH30814.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig-cl.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 2.
DR      SMART; SM00406; IGV; 1.
DR      SMART; SM00407; IGV; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match      78.6%; Score 892.5; DB 4; Length 239;
Best Local Similarity 79.0%; Pred. No. 5.4e-74;
Matches 173; Conservative 17; Mismatches 28; Indels 1; Gaps 1;

.Qy      1  DIQLTQSPSSLSASVGDVRTITCRASQSDY-DGDSYMNWYQKPGKAPKLLIYAASYLE 59
      21  DIVMTQSLPLVTPGEPASISCRSSQSLHSDGYNLWYLOKPGQSPQLLIYLGSNRA 80
      60  SGVPSRFSGSGSGTDFTLTITSLQPEDFATYICQOSHEDPYTFGQGTKEIKRTVAAPSV 119
      81  SGVPDRFSGSGSGTDFTLKISKVEADVGIIYCMQGLTPQTTFGQGTKEIKRTVAAPSV 140
      120  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
      141  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200

Db      60  SGVPSRFSGSGSGTDFTLTITSLQPEDFATYICQOSHEDPYTFGQGTKEIKRTVAAPSV 119
      81  SGVPDRFSGSGSGTDFTLKISKVEADVGIIYCMQGLTPQTTFGQGTKEIKRTVAAPSV 140
      120  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
      141  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200

.Qy      180  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
      201  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

Db      180  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
      201  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3
Q8TCD0
ID      Q8TCD0      PRELIMINARY;      PRT;      239 AA.
AC      Q8TCD0;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RA      Strausberg R.;
RL      Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC022362; AAH22362.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 2.
DR      SMART; SM00406; IGV; 1.
DR      SMART; SM00407; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match      78.5%; Score 891.5; DB 4; Length 239;
Best Local Similarity 77.2%; Pred. No. 6.6e-74;
Matches 169; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

.Qy      1  DIQLTQSPSSLSASVGDVRTITCRASQSDY-DGDSYMNWYQKPGKAPKLLIYAASYLE 59
      21  DIVMTQSLPLVTPGEPASISCRSSQSLVSDGNTYLNWFCQRPQSPRLIYKVSNRD 80
      60  SGVPSRFSGSGSGTDFTLTITSLQPEDFATYICQOSHEDPYTFGQGTKEIKRTVAAPSV 119
      81  SGVPDRFSGSGSGTDFTLKIRVEAEDVGIVCMQGTWPSTFGQGTKEIKRTVAAPSV 140
      120  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
      141  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200

.Qy      180  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
      201  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

Db      180  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
      201  SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4
Q8R062
ID      Q8R062      PRELIMINARY;      PRT;      234 AA.
AC      Q8R062;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical 25.9 kDa protein.
OS      Mus musculus (Mouse)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Colon;
RA      Strausberg R.;
RL      Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC027418; AAH27418.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 2.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match      65.0%; Score 738; DB 11; Length 234;
Best Local Similarity 64.2%; Pred. No. 8.2e-60;
Matches 140; Conservative 29; Mismatches 45; Indels 4; Gaps 1;

.Qy      1  DIQLTQSPSSLSASVGDVRTITCRASQSDY-DGDSYMNWYQKPGKAPKLLIYAASYLE 60
      21  DIVMTQSLPLVTPGEPASISCRSSQSLHSDGYNLWYLOKPGQSPQLLIYLGSNRA 80
      60  SGVPSRFSGSGSGTDFTLTITSLQPEDFATYICQOSHEDPYTFGQGTKEIKRTVAAPSV 119
      81  SGVPDRFSGSGSGTDFTLKISKVEADVGIIYCMQGLTPQTTFGQGTKEIKRTVAAPSV 140
      120  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
      141  FIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200

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Db 21 DIQMTQTSSLSASLGDRVTITCRASQSGI----SNLYNMWYQKPGDGTVKLLIYTTSLHS 76
QY 61 GVPFRSGSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFGGTKVEIKRTVAAPS VF 120
Db 77 GVPFRSGSGSGHYSLTISNLEPEDINAYVCOQYQSFPTFGSGTKLEIKRADAAPT VS 136
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPRKAYQKVDNALQSGNSQESVTEQDSKDSYSL S 180
Db 137 IFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTQDSKDSY S 196
QY 181 STLTSLKADYEKKHYACEVTHOGLSPVTKSFNRGEC 218
Db 197 STLTSLKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 5
Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015292; AAH15292.1;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR001865; Ribosomal_S2.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00962; RIBOSOMAL_S2.1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0B6EB7812D2 CRC64;

Query Match 64.6%; Score 733; DB 11; Length 234;
Best Local Similarity 63.3%; Pred. No. 2.4e-59;
Matches 138; Conservative 31; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQMTQTSSLSASLGDRVTITCRASQSDYDGDYNNWYQKPGKAPKLLIYAASVLES 60
Db 21 DIQMTQTSSLSASLGDRVTITCRASQDI----SNLYNMWYQKPGDGTVKLLIYTTSLYL 76
QY 61 GVPFRSGSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFGGTKVEIKRTVAAPS VF 120
Db 77 GVPFRSGSGSGHYSLTISNLEPEDINAYVCOQYQSFPTFGSGTKLEIKRADAAPT VS 136
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPRKAYQKVDNALQSGNSQESVTEQDSKDSYSL S 180
Db 137 IFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTQDSKDSY S 196
QY 181 STLTSLKADYEKKHYACEVTHOGLSPVTKSFNRGEC 218
Db 197 STLTSLKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 6
Q91WS9
ID Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013496; AAH13496.1;
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 64.5%; Score 732; DB 11; Length 233;
Best Local Similarity 64.2%; Pred. No. 2.9e-59;
Matches 140; Conservative 28; Mismatches 46; Indels 4; Gaps 1;

QY 1 DIQMTQTSSLSASLGDRVTITCRASQSDYDGDYNNWYQKPGKAPKLLIYAASVLES 60
Db 20 DIQMTQTSSLSASLGDRVTITCRASQSGI----ANYLNMWYQKPGDGTVKLLIYTTSLHS 75
QY 61 GVPFRSGSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFGGTKVEIKRTVAAPS VF 120
Db 76 GVPFRSGSGSGDYSLTISNLEPEDINAYVCOQYQYRLPWTFTGGTKLEIKRADAAPT VS 135
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPRKAYQKVDNALQSGNSQESVTEQDSKDSYSL S 180
Db 136 IFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRONGVLSNWTQDSKDSY S 195
QY 181 STLTSLKADYEKKHYACEVTHOGLSPVTKSFNRGEC 218
Db 196 STLTSLKDEYERHNSYTCETHKTSPIVKSFNREC 233

RESULT 7
Q9RIA5
ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ektamoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, ics light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1;
DR HSP: P01679; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

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Query Match      64.4%; Score 731; DB 11; Length 214;
Best Local Similarity 63.3%; Pred. No. 3.2e-59;
Matches 138; Conservative 31; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQLTSPSSLSASVGDRTVITCRASQSDYDGDGYNNWYQKPGKAPKLLIYAASYLE 60
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 1 DIQLTSPSSLSASVGDRTVITCRASQSDYDGDGYNNWYQKPGKAPKLLIYAASYLE 56
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||

QY 61 GVPSPSSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFQGGTKVEIKRTVAAPSV 120
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 57 GVPSPSSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFQGGTKVEIKRTVAAPSV 116

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 117 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176

QY 181 STLTSLKADYEKKHVKVACEVTHOGLSSPVTKSFNRGEC 218
    ||||| :||: ||||| ||||| :||: ||||| ||||| ||||| ||||| |||||
Db 177 STLTSLKADYEKKHVKVACEVTHOGLSSPVTKSFNRGEC 214

RESULT 8
Q8VCP0 PRELIMINARY; PRT; 234 AA.
ID Q8VCP0
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DE 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match      64.3%; Score 730; DB 11; Length 234;
Best Local Similarity 63.8%; Pred. No. 4.4e-59;
Matches 139; Conservative 29; Mismatches 46; Indels 4; Gaps 1;

QY 1 DIQLTSPSSLSASVGDRTVITCRASQSDYDGDGYNNWYQKPGKAPKLLIYAASYLE 60
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 21 DIQLTSPSSLSASVGTITCRASENI----YSYLANWYQKQKSPQLLYNKTAD 76
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||

QY 61 GVPSPSSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFQGGTKVEIKRTVAAPSV 120
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 77 GVPSPSSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFQGGTKVEIKRTVAAPSV 136

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 137 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 196

QY 181 STLTSLKADYEKKHVKVACEVTHOGLSSPVTKSFNRGEC 218
    ||||| :||: ||||| ||||| :||: ||||| ||||| ||||| ||||| |||||
Db 197 STLTSLKADYEKKHVKVACEVTHOGLSSPVTKSFNRGEC 234

RESULT 9
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1;
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match      62.0%; Score 703.5; DB 11; Length 238;
Best Local Similarity 59.8%; Pred. No. 1.2e-56;
Matches 131; Conservative 34; Mismatches 53; Indels 1; Gaps 1;

QY 1 DIQLTSPSSLSASVGDRTVITCRASQSDYDGDGYNNWYQKPGKAPKLLIYAASYLE 59
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 20 DVYMTPLSLPLVSLGDAQSISCRSSQSVIHSGNTLYLEWYQKPGQSPKLLIYKVSNR 79
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||

QY 60 SGVPSRFSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFQGGTKVEIKRTVAAPSV 119
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 80 SGVPSRFSGSGDFTLTITSSLOPEDFATYVCOQSHEDPYTFQGGTKVEIKRTVAAPSV 139

QY 120 FIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
    ||||| ||||| :||:|||||:||||: ||||| ||||| ||||| ||||| |||||
Db 140 FIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 199

QY 180 SSSLTSLKADYEKKHVKVACEVTHOGLSSPVTKSFNRGEC 218
    ||||| :||: ||||| ||||| :||: ||||| ||||| ||||| ||||| |||||
Db 200 SSSLTSLKADYEKKHVKVACEVTHOGLSSPVTKSFNRGEC 238

RESULT 10
Q8VCI6 PRELIMINARY; PRT; 238 AA.
ID Q8VCI6
AC Q8VCI6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match      61.1%; Score 693.5; DB 11; Length 238;
Best Local Similarity 59.8%; Pred. No. 1e-55;
Matches 131; Conservative 34; Mismatches 53; Indels 1; Gaps 1;
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